

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 21 Seconds
(without alignments)
2678.030 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DANKSEVAHRKDLGEENFK.....TCFAEGKLVLAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	609	1 ABHUS	serum albumin prec
2	2942	94.8	600	2 A47391	serum albumin prec
3	2820	84.4	608	2 S7632	serum albumin prec
4	2475.5	79.8	607	1 ABHOS	serum albumin prec
5	2446.5	78.8	607	1 ABBOS	serum albumin prec
6	2432.5	78.4	607	1 ABRHS	serum albumin prec
7	2426	78.2	608	1 ABRTS	serum albumin prec
8	2411.5	77.7	605	1 ABPGS	serum albumin prec
9	2387	76.9	609	2 JC5838	albumin - Mongolia
10	1861	60.0	453	2 A05139	serum albumin - mo
11	1557.5	50.2	615	1 ABCSHS	serum albumin prec
12	1253.5	40.4	609	2 JC4258	alpha-fetoprotein
13	1249.5	40.3	609	1 FPHU	alpha-fetoprotein
14	1242.5	40.0	609	1 FPGO	alpha-fetoprotein
15	1205	38.8	607	1 ABXL72	74K albumin prec
16	1181.5	38.1	265	2 I46986	albumin - dog (ira
17	1175.5	37.9	608	1 ABXL68	68K serum albumin
18	1084	34.9	605	1 FPM5	alpha-fetoprotein
19	1067	34.4	611	1 FPR7	alpha-fetoprotein
20	1055	34.0	599	1 A34906	afamin precursor -
21	928.5	29.9	614	2 S59517	serum albumin prec
22	928	29.9	608	2 A53195	afamin precursor -
23	747.5	24.1	608	1 ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1 ABONS2	serum albumin 2 pr
25	699	22.5	382	2 A37253	serum albumin - bu
26	440.5	14.2	1423	1 S27941	serum albumin - se
27	386	12.4	474	1 VYHUI	vitamin D-binding
28	385	12.4	476	1 VVRTD	vitamin D-binding
29	372	12.0	472	1 A35327	vitamin D-binding

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

N:Contains: Kinetensin

C:Species: Homo sapiens (man)

C:Date: 29-Jul-1981 #sequence-revision 31-Jan-1997 #text-change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Se

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, K, 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:C

R:Dugaiczky, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, 'G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <ORA>

A:Cross-references: GB:M13075; NID:g178330; PIDN:AAA51688.1; PID:g553173

R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fam

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 282-290, 'KSRFDLQ' <WAT>

A:Cross-references: GB:S69192; NID:g546032; PIDN:AAB30282.1; PID:g546033

A:Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putn

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carb

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRRVKNLIQVKLP' <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

THIS PAGE BLANK (USPTO)

A:Note: this frame-shift variant is designated albumin Bazzano; four additional variants submitted to the EMBL Data Library, March 1995
 A:Reference number: G08292
 A:Accession: G01747
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-120, 'G', 122-455 <MEN>
 A:Cross-references: EMBL:U22361; NID:G763428; PIDN:AAA64922.1; PID:G763431
 R:Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
 Biochem. J. 308, 321-325, 1995
 A:Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex2
 A:Reference number: S55314; MUID:95275251; PMID:7755581
 A:Accession: S55314
 A:Molecule type: protein
 A:Residues: 19-27 <LED>
 R:Meloun, B.; Moravek, L.; Kostka, V.
 FEBS Lett. 58, 134-137, 1975
 A:Title: Complete amino acid sequence of human serum albumin.
 A:Reference number: A91420; MUID:76187907; PMID:1225573
 A:Accession: A91420
 A:Molecule type: protein
 A:Residues: 25-117, 'EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-396, 'R', 397-400, 'D', 401-402, 'E', 403-404, 'K', 405-406, 'R', 407-408, 'D', 409-410, 'E', 411-412, 'K', 413-414, 'R', 415-416, 'K', 417-418, 'R', 419-420, 'K', 421-422, 'R', 423-424, 'K', 425-426, 'R', 427-428, 'K', 429-430, 'R', 431-432, 'K', 433-434, 'R', 435-436, 'K', 437-438, 'R', 439-440, 'K', 441-442, 'R', 443-444, 'K', 445-446, 'R', 447-448, 'K', 449-450, 'R', 451-452, 'K', 453-454, 'R', 455-456, 'K', 457-458, 'R', 459-460, 'K', 461-462, 'R', 463-464, 'K', 465-466, 'R', 467-468, 'K', 469-470, 'R', 471-472, 'K', 473-474, 'R', 475-476, 'K', 477-478, 'R', 479-480, 'K', 481-482, 'R', 483-484, 'K', 485-486, 'R', 487-488, 'K', 489-490, 'R', 491-492, 'K', 493-494, 'R', 495-496, 'K', 497-498, 'R', 499-500, 'K', 501-502, 'R', 503-504, 'K', 505-506, 'R', 507-508, 'K', 509-510, 'R', 511-512, 'K', 513-514, 'R', 515-516, 'K', 517-518, 'R', 519-520, 'K', 521-522, 'R', 523-524, 'K', 525-526, 'R', 527-528, 'K', 529-530, 'R', 531-532, 'K', 533-534, 'R', 535-536, 'K', 537-538, 'R', 539-540, 'K', 541-542, 'R', 543-544, 'K', 545-546, 'R', 547-548, 'K', 549-550, 'R', 551-552, 'K', 553-554, 'R', 555-556, 'K', 557-558, 'R', 559-560, 'K', 561-562, 'R', 563-564, 'K', 565-566, 'R', 567-568, 'K', 569-570, 'R', 571-572, 'K', 573-574, 'R', 575-576, 'K', 577-578, 'R', 579-580, 'K', 581-582, 'R', 583-584, 'K', 585-586, 'R', 587-588, 'K', 589-590, 'R', 591-592, 'K', 593-594, 'R', 595-596, 'K', 597-598, 'R', 599-600, 'K', 601-602, 'R', 603-604, 'K', 605-606, 'R', 607-608, 'K', 609-610, 'R', 611-612, 'K', 613-614, 'R', 615-616, 'K', 617-618, 'R', 619-620, 'K', 621-622, 'R', 623-624, 'K', 625-626, 'R', 627-628, 'K', 629-630, 'R', 631-632, 'K', 633-634, 'R', 635-636, 'K', 637-638, 'R', 639-640, 'K', 641-642, 'R', 643-644, 'K', 645-646, 'R', 647-648, 'K', 649-650, 'R', 651-652, 'K', 653-654, 'R', 655-656, 'K', 657-658, 'R', 659-660, 'K', 661-662, 'R', 663-664, 'K', 665-666, 'R', 667-668, 'K', 669-670, 'R', 671-672, 'K', 673-674, 'R', 675-676, 'K', 677-678, 'R', 679-680, 'K', 681-682, 'R', 683-684, 'K', 685-686, 'R', 687-688, 'K', 689-690, 'R', 691-692, 'K', 693-694, 'R', 695-696, 'K', 697-698, 'R', 699-700, 'K', 701-702, 'R', 703-704, 'K', 705-706, 'R', 707-708, 'K', 709-710, 'R', 711-712, 'K', 713-714, 'R', 715-716, 'K', 717-718, 'R', 719-720, 'K', 721-722, 'R', 723-724, 'K', 725-726, 'R', 727-728, 'K', 729-730, 'R', 731-732, 'K', 733-734, 'R', 735-736, 'K', 737-738, 'R', 739-740, 'K', 741-742, 'R', 743-744, 'K', 745-746, 'R', 747-748, 'K', 749-750, 'R', 751-752, 'K', 753-754, 'R', 755-756, 'K', 757-758, 'R', 759-760, 'K', 761-762, 'R', 763-764, 'K', 765-766, 'R', 767-768, 'K', 769-770, 'R', 771-772, 'K', 773-774, 'R', 775-776, 'K', 777-778, 'R', 779-780, 'K', 781-782, 'R', 783-784, 'K', 785-786, 'R', 787-788, 'K', 789-790, 'R', 791-792, 'K', 793-794, 'R', 795-796, 'K', 797-798, 'R', 799-800, 'K', 801-802, 'R', 803-804, 'K', 805-806, 'R', 807-808, 'K', 809-810, 'R', 811-812, 'K', 813-814, 'R', 815-816, 'K', 817-818, 'R', 819-820, 'K', 821-822, 'R', 823-824, 'K', 825-826, 'R', 827-828, 'K', 829-830, 'R', 831-832, 'K', 833-834, 'R', 835-836, 'K', 837-838, 'R', 839-840, 'K', 841-842, 'R', 843-844, 'K', 845-846, 'R', 847-848, 'K', 849-850, 'R', 851-852, 'K', 853-854, 'R', 855-856, 'K', 857-858, 'R', 859-860, 'K', 861-862, 'R', 863-864, 'K', 865-866, 'R', 867-868, 'K', 869-870, 'R', 871-872, 'K', 873-874, 'R', 875-876, 'K', 877-878, 'R', 879-880, 'K', 881-882, 'R', 883-884, 'K', 885-886, 'R', 887-888, 'K', 889-890, 'R', 891-892, 'K', 893-894, 'R', 895-896, 'K', 897-898, 'R', 899-900, 'K', 901-902, 'R', 903-904, 'K', 905-906, 'R', 907-908, 'K', 909-910, 'R', 911-912, 'K', 913-914, 'R', 915-916, 'K', 917-918, 'R', 919-920, 'K', 921-922, 'R', 923-924, 'K', 925-926, 'R', 927-928, 'K', 929-930, 'R', 931-932, 'K', 933-934, 'R', 935-936, 'K', 937-938, 'R', 939-940, 'K', 941-942, 'R', 943-944, 'K', 945-946, 'R', 947-948, 'K', 949-950, 'R', 951-952, 'K', 953-954, 'R', 955-956, 'K', 957-958, 'R', 959-960, 'K', 961-962, 'R', 963-964, 'K', 965-966, 'R', 967-968, 'K', 969-970, 'R', 971-972, 'K', 973-974, 'R', 975-976, 'K', 977-978, 'R', 979-980, 'K', 981-982, 'R', 983-984, 'K', 985-986, 'R', 987-988, 'K', 989-990, 'R', 991-992, 'K', 993-994, 'R', 995-996, 'K', 997-998, 'R', 999-1000, 'K', 1001-1002, 'R', 1003-1004, 'K', 1005-1006, 'R', 1007-1008, 'K', 1009-1010, 'R', 1011-1012, 'K', 1013-1014, 'R', 1015-1016, 'K', 1017-1018, 'R', 1019-1020, 'K', 1021-1022, 'R', 1023-1024, 'K', 1025-1026, 'R', 1027-1028, 'K', 1029-1030, 'R', 1031-1032, 'K', 1033-1034, 'R', 1035-1036, 'K', 1037-1038, 'R', 1039-1040, 'K', 1041-1042, 'R', 1043-1044, 'K', 1045-1046, 'R', 1047-1048, 'K', 1049-1050, 'R', 1051-1052, 'K', 1053-1054, 'R', 1055-1056, 'K', 1057-1058, 'R', 1059-1060, 'K', 1061-1062, 'R', 1063-1064, 'K', 1065-1066, 'R', 1067-1068, 'K', 1069-1070, 'R', 1071-1072, 'K', 1073-1074, 'R', 1075-1076, 'K', 1077-1078, 'R', 1079-1080, 'K', 1081-1082, 'R', 1083-1084, 'K', 1085-1086, 'R', 1087-1088, 'K', 1089-1090, 'R', 1091-1092, 'K', 1093-1094, 'R', 1095-1096, 'K', 1097-1098, 'R', 1099-1100, 'K', 1101-1102, 'R', 1103-1104, 'K', 1105-1106, 'R', 1107-1108, 'K', 1109-1110, 'R', 1111-1112, 'K', 1113-1114, 'R', 1115-1116, 'K', 1117-1118, 'R', 1119-1120, 'K', 1121-1122, 'R', 1123-1124, 'K', 1125-1126, 'R', 1127-1128, 'K', 1129-1130, 'R', 1131-1132, 'K', 1133-1134, 'R', 1135-1136, 'K', 1137-1138, 'R', 1139-1140, 'K', 1141-1142, 'R', 1143-1144, 'K', 1145-1146, 'R', 1147-1148, 'K', 1149-1150, 'R', 1151-1152, 'K', 1153-1154, 'R', 1155-1156, 'K', 1157-1158, 'R', 1159-1160, 'K', 1161-1162, 'R', 1163-1164, 'K', 1165-1166, 'R', 1167-1168, 'K', 1169-1170, 'R', 1171-1172, 'K', 1173-1174, 'R', 1175-1176, 'K', 1177-1178, 'R', 1179-1180, 'K', 1181-1182, 'R', 1183-1184, 'K', 1185-1186, 'R', 1187-1188, 'K', 1189-1190, 'R', 1191-1192, 'K', 1193-1194, 'R', 1195-1196, 'K', 1197-1198, 'R', 1199-1200, 'K', 1201-1202, 'R', 1203-1204, 'K', 1205-1206, 'R', 1207-1208, 'K', 1209-1210, 'R', 1211-1212, 'K', 1213-1214, 'R', 1215-1216, 'K', 1217-1218, 'R', 1219-1220, 'K', 1221-1222, 'R', 1223-1224, 'K', 1225-1226, 'R', 1227-1228, 'K', 1229-1230, 'R', 1231-1232, 'K', 1233-1234, 'R', 1235-1236, 'K', 1237-1238, 'R', 1239-1240, 'K', 1241-1242, 'R', 1243-1244, 'K', 1245-1246, 'R', 1247-1248, 'K', 1249-1250, 'R', 1251-1252, 'K', 1253-1254, 'R', 1255-1256, 'K', 1257-1258, 'R', 1259-1260, 'K', 1261-1262, 'R', 1263-1264, 'K', 1265-1266, 'R', 1267-1268, 'K', 1269-1270, 'R', 1271-1272, 'K', 1273-1274, 'R', 1275-1276, 'K', 1277-1278, 'R', 1279-1280, 'K', 1281-1282, 'R', 1283-1284, 'K', 1285-1286, 'R', 1287-1288, 'K', 1289-1290, 'R', 1291-1292, 'K', 1293-1294, 'R', 1295-1296, 'K', 1297-1298, 'R', 1299-1300, 'K', 1301-1302, 'R', 1303-1304, 'K', 1305-1306, 'R', 1307-1308, 'K', 1309-1310, 'R', 1311-1312, 'K', 1313-1314, 'R', 1315-1316, 'K', 1317-1318, 'R', 1319-1320, 'K', 1321-1322, 'R', 1323-1324, 'K', 1325-1326, 'R', 1327-1328, 'K', 1329-1330, 'R', 1331-1332, 'K', 1333-1334, 'R', 1335-1336, 'K', 1337-1338, 'R', 1339-1340, 'K', 1341-1342, 'R', 1343-1344, 'K', 1345-1346, 'R', 1347-1348, 'K', 1349-1350, 'R', 1351-1352, 'K', 1353-1354, 'R', 1355-1356, 'K', 1357-1358, 'R', 1359-1360, 'K', 1361-1362, 'R', 1363-1364, 'K', 1365-1366, 'R', 1367-1368, 'K', 1369-1370, 'R', 1371-1372, 'K', 1373-1374, 'R', 1375-1376, 'K', 1377-1378, 'R', 1379-1380, 'K', 1381-1382, 'R', 1383-1384, 'K', 1385-1386, 'R', 1387-1388, 'K', 1389-1390, 'R', 1391-1392, 'K', 1393-1394, 'R', 1395-1396, 'K', 1397-1398, 'R', 1399-1400, 'K', 1401-1402, 'R', 1403-1404, 'K', 1405-1406, 'R', 1407-1408, 'K', 1409-1410, 'R', 1411-1412, 'K', 1413-1414, 'R', 1415-1416, 'K', 1417-1418, 'R', 1419-1420, 'K', 1421-1422, 'R', 1423-1424, 'K', 1425-1426, 'R', 1427-1428, 'K', 1429-1430, 'R', 1431-1432, 'K', 1433-1434, 'R', 1435-1436, 'K', 1437-1438, 'R', 1439-1440, 'K', 1441-1442, 'R', 1443-1444, 'K', 1445-1446, 'R', 1447-1448, 'K', 1449-1450, 'R', 1451-1452, 'K', 1453-1454, 'R', 1455-1456, 'K', 1457-1458, 'R', 1459-1460, 'K', 1461-1462, 'R', 1463-1464, 'K', 1465-1466, 'R', 1467-1468, 'K', 1469-1470, 'R', 1471-1472, 'K', 1473-1474, 'R', 1475-1476, 'K', 1477-1478, 'R', 1479-1480, 'K', 1481-1482, 'R', 1483-1484, 'K', 1485-1486, 'R', 1487-1488, 'K', 1489-1490, 'R', 1491-1492, 'K', 1493-1494, 'R', 1495-1496, 'K', 1497-1498, 'R', 1499-1500, 'K', 1501-1502, 'R', 1503-1504, 'K', 1505-1506, 'R', 1507-1508, 'K', 1509-1510, 'R', 1511-1512, 'K', 1513-1514, 'R', 1515-1516, 'K', 1517-1518, 'R', 1519-1520, 'K', 1521-1522, 'R', 1523-1524, 'K', 1525-1526, 'R', 1527-1528, 'K', 1529-1530, 'R', 1531-1532, 'K', 1533-1534, 'R', 1535-1536, 'K', 1537-1538, 'R', 1539-1540, 'K', 1541-1542, 'R', 1543-1544, 'K', 1545-1546, 'R', 1547-1548, 'K', 1549-1550, 'R', 1551-1552, 'K', 1553-1554, 'R', 1555-1556, 'K', 1557-1558, 'R', 1559-1560, 'K', 1561-1562, 'R', 1563-1564, 'K', 1565-1566, 'R', 1567-1568, 'K', 1569-1570, 'R', 1571-1572, 'K', 1573-1574, 'R', 1575-1576, 'K', 1577-1578, 'R', 1579-1580, 'K', 1581-1582, 'R', 1583-1584, 'K', 1585-1586, 'R', 1587-1588, 'K', 1589-1590, 'R', 1591-1592, 'K', 1593-1594, 'R', 1595-1596, 'K', 1597-1598, 'R', 1599-1600, 'K', 1601-1602, 'R', 1603-1604, 'K', 1605-1606, 'R', 1607-1608, 'K', 1609-1610, 'R', 1611-1612, 'K', 1613-1614, 'R', 1615-1616, 'K', 1617-1618, 'R', 1619-1620, 'K', 1621-1622, 'R', 1623-1624, 'K', 1625-1626, 'R', 1627-1628, 'K', 1629-1630, 'R', 1631-1632, 'K', 1633-1634, 'R', 1635-1636, 'K', 1637-1638, 'R', 1639-1640, 'K', 1641-1642, 'R', 1643-1644, 'K', 1645-1646, 'R', 1647-1648, 'K', 1649-1650, 'R', 1651-1652, 'K', 1653-1654, 'R', 1655-1656, 'K', 1657-1658, 'R', 1659-1660, 'K', 1661-1662, 'R', 1663-1664, 'K', 1665-1666, 'R', 1667-1668, 'K', 1669-1670, 'R', 1671-1672, 'K', 1673-1674, 'R', 1675-1676, 'K', 1677-1678, 'R', 1679-1680, 'K', 1681-1682, 'R', 1683-1684, 'K', 1685-1686, 'R', 1687-1688, 'K', 1689-1690, 'R', 1691-1692, 'K', 1693-1694, 'R', 1695-1696, 'K', 1697-1698, 'R', 1699-1700, 'K', 1701-1702, 'R', 1703-1704, 'K', 1705-1706, 'R', 1707-1708, 'K', 1709-1710, 'R', 1711-1712, 'K', 1713-1714, 'R', 1715-1716, 'K', 1717-1718, 'R', 1719-1720, 'K', 1721-1722, 'R', 1723-1724, 'K', 1725-1726, 'R', 1727-1728, 'K', 1729-1730, 'R', 1731-1732, 'K', 1733-1734, 'R', 1735-1736, 'K', 1737-1738, 'R', 1739-1740, 'K', 1741-1742, 'R', 1743-1744, 'K', 1745-1746, 'R', 1747-1748, 'K', 1749-1750, 'R', 1751-1752, 'K', 1753-1754, 'R', 1755-1756, 'K', 1757-1758, 'R', 1759-1760, 'K', 1761-1762, 'R', 1763-1764, 'K', 1765-1766, 'R', 1767-1768, 'K', 1769-1770, 'R', 1771-1772, 'K', 1773-1774, 'R', 1775-1776, 'K', 1777-1778, 'R', 1779-1780, 'K', 1781-1782, 'R', 1783-1784, 'K', 1785-1786, 'R', 1787-1788, 'K', 1789-1790, 'R', 1791-1792, 'K', 1793-1794, 'R', 1795-1796, 'K', 1797-1798, 'R', 1799-1800, 'K', 1801-1802, 'R', 1803-1804, 'K', 1805-1806, 'R', 1807-1808, 'K', 1809-1810, 'R', 1811-1812, 'K', 1813-1814, 'R', 1815-1816, 'K', 1817-1818, 'R', 1819-1820, 'K', 1821-1822, 'R', 1823-1824, 'K', 1825-1826, 'R', 1827-1828, 'K', 1829-1830, 'R', 1831-1832, 'K', 1833-1834, 'R', 1835-1836, 'K', 1837-1838, 'R', 1839-1840, 'K', 1841-1842, 'R', 1843-1844, 'K', 1845-1846, 'R', 1847-1848, 'K', 1849-1850, 'R', 1851-1852, 'K', 1853-1854, 'R', 1855-1856, 'K', 1857-1858, 'R', 1859-1860, 'K', 1861-1862, 'R', 1863-1864, 'K', 1865-1866, 'R', 1867-1868, 'K', 1869-1870, 'R', 1871-1872, 'K', 1873-1874, 'R', 1875-1876, 'K', 1877-1878, 'R', 1879-1880, 'K', 1881-1882, 'R', 1883-1884, 'K', 1885-1886, 'R', 1887-1888, 'K', 1889-1890, 'R', 1891-1892, 'K', 1893-1894, 'R', 1895-1896, 'K', 1897-1898, 'R', 1899-1900, 'K', 1901-1902, 'R', 1903-1904, 'K', 1905-1906, 'R', 1907-1908, 'K', 1909-1910, 'R', 1911-1912, 'K', 1913-1914, 'R', 1915-1916, 'K', 1917-1918, 'R', 1919-1920, 'K', 1921-1922, 'R', 1923-1924, 'K', 1925-1926, 'R', 1927-1928, 'K', 1929-1930, 'R', 1931-1932, 'K', 1933-1934, 'R', 1935-1936, 'K', 1937-1938, 'R', 1939-1940, 'K', 1941-1942, 'R', 1943-1944, 'K', 1945-1946, 'R', 1947-1948, 'K', 1949-1950, 'R', 1951-1952, 'K', 1953-1954, 'R', 1955-1956, 'K', 1957-1958, 'R', 1959-1960, 'K', 1961-1962, 'R', 1963-1964, 'K', 1965-1966, 'R', 1967-1968, 'K', 1969-1970, 'R', 1971-1972, 'K', 1973-1974, 'R', 1975-1976, 'K', 1977-1978, 'R', 1979-1980, 'K', 1981-1982, 'R', 1983-1984, 'K', 1985-1986, 'R', 1987-1988, 'K', 1989-1990, 'R', 1991-1992, 'K', 1993-1994, 'R', 1995-1996, 'K', 1997-1998, 'R', 1999-2000, 'K', 2001-2002, 'R', 2003-2004, 'K', 2005-2006, 'R', 2007-2008, 'K', 2009-2010, 'R', 2011-2012, 'K', 2013-2014, 'R', 2015-2016, 'K', 2017-2018, 'R', 2019-2020, 'K', 2021-2022, 'R', 2023-2024, 'K', 2025-2026, 'R', 2027-2028, 'K', 2029-2030, 'R', 2031-2032, 'K', 2033-2034, 'R', 2035-2036, 'K', 2037-2038, 'R', 2039-2040, 'K', 2041-2042, 'R', 2043-2044, 'K', 2045-2046, 'R', 2047-2048, 'K', 2049-2050, 'R', 2051-2052, 'K', 2053-2054, 'R', 2055-2056, 'K', 2057-2058, 'R', 2059-2060, 'K', 2061-2062, 'R', 2063-2064, 'K', 2065-2066, 'R', 2067-2068, 'K', 2069-2070, 'R', 2071-2072, 'K', 2073-2074, 'R', 2075-2076, 'K', 2077-2078, 'R', 2079-2080, 'K', 2081-2082, 'R', 2083-2084, 'K', 2085-2086, 'R', 2087-2088, 'K', 2089-2090, 'R', 2091-2092, 'K', 2093-2094, 'R', 2095-2096, 'K', 2097-2098, 'R', 2099-2100, 'K', 2101-2102, 'R', 2103-2104, 'K', 2105-2106, 'R', 2107-2108, 'K', 2109-2110, 'R', 2111-2112, 'K', 2113-2114, 'R', 2115-2116, 'K', 2117-2118, 'R', 2119-2120, 'K', 2121-2122, 'R', 2123-2124, 'K', 2125-2126, 'R', 2127-2128, 'K', 2129-2130, 'R', 2131-2132, 'K', 2133-2134, 'R', 2135-2136, 'K', 2137-2138, 'R', 2139-2140, 'K', 2141-2142, 'R', 2143-2144, 'K', 2145-2146, 'R', 2147-2148, 'K', 2149-2150, 'R

THIS PAGE BLANK (USPTO)

F:166-174/Product: kinetensin #status experimental <KIP>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA2>
 F:27/Binding site: copper (His) #status predicted
 F:77-86.99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,413-592/Domain: serum albumin repeat homology <SA2>
 F:214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0%; Score 3103; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 7.4e-198;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGEENFKALVLIATFAOYLQOCPEFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 25 DAHSEVAHFRKDLGEENFKALVLIATFAOYLQOCPEFEDHVKLVNEVTEFAKTCVADESAAE 84
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLVRPEV 120
 DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLVRPEV 144
 QY 121 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAFAEVECCQAADKAACLLP 180
 DB 145 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAFAEVECCQAADKAACLLP 204
 QY 181 KLDELDEGRASSAKQRLKASLOKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 DB 205 KLDELDEGRASSAKQRLKASLOKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 264
 QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVENDEMPA 300
 DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVENDEMPA 324
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVLLRLAKTYETTLTK 360
 DB 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVLLRLAKTYETTLTK 384
 QY 361 CAADPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVPOVST 420
 DB 385 CAADPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVPOVST 444
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 504
 QY 481 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKOTALVELVYKHKPKAT 540
 DB 505 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKOTALVELVYKHKPKAT 564
 QY 541 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAALGL 585
 DB 565 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAALGL 609

RESULT 2

A47391
 serum albumin precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C:Accession: A47391
 R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
 A:Title: cDNA and protein sequence of polymorphic macaque albumins that differ in biliru-
 A:Reference number: A47391; MUID:93211971; PMID:8460152
 A:Contents: B/B homozygote
 A:Accession: A47391
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-600 <WAT>
 A:Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBI:128281)
 C:Superfamily: serum albumin; serum albumin repeat homology
 F:21-194/Domain: serum albumin repeat homology <SA1>
 F:213-386/Domain: serum albumin repeat homology <SA2>

F:405-584/Domain: serum albumin repeat homology <SA3>

Query Match 94.8%; Score 2942; DB 2; Length 600;
 Best Local Similarity 93.5%; Pred. No. 3.3e-187;
 Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGEENFKALVLIATFAOYLQOCPEFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 17 DTHSEVAHFRKDLGEENFKALVLIATFAOYLQOCPEFEDHVKLVNEVTEFAKTCVADESAAE 76
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLVRPEV 120
 DB 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLVRPEV 136
 QY 121 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAFAEVECCQAADKAACLLP 180
 DB 137 DVMCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAFAEVECCQAADKAACLLP 196
 QY 181 KLDELDEGRASSAKQRLKASLOKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 DB 197 KLDELDEGRASSAKQRLKASLOKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 256
 QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVENDEMPA 300
 DB 257 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVENDEMPA 316
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVLLRLAKTYETTLTK 360
 DB 317 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYIYARRHPDYSVLLRLAKTYETTLTK 376
 QY 361 CAADPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVPOVST 420
 DB 377 CAADPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVPOVST 436
 QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 437 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 496
 QY 481 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKOTALVELVYKHKPKAT 540
 DB 497 LVNRRPCFSALEVDETVVPKEFNAETTFHADICTLSEKERQIKKOTALVELVYKHKPKAT 556
 QY 541 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAAL 583
 DB 557 KEOLKAVMDFAAFVEKCKRADDKTCFAEEGKKLVAAASQAAL 599

RESULT 3

S57632
 serum albumin precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
 C:Accession: JCA4660; S57632
 R:Hilger, C.; Grigioni, F.; Hentges, F.
 Gene 169, 295-296, 1996
 A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
 A:Reference number: JCA4660; MUID:96194824; PMID:8647469
 A:Accession: JCA4660
 A:Molecule type: mRNA
 A:Residues: 1-608 <HI2>
 A:Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
 A:Experimental source: liver
 A:Comment: This protein is the major protein component in plasma. It functions as a p

C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: liver; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRP>
 F:25-608/Product: serum albumin #status predicted <MAT>
 F:29-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>

THIS PAGE BLANK (USPTO)

QY 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASQKFGKRAFAKAWARLSORFFKAEFVSKLVDTLTK 240
Db 181 KLDELDEGKASSAKQRLKASQKFGKRAFAKAWARLSORFFKAEFVSKLVDTLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
Db 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
QY 361 CAADPHCEYAKVDFEFLVPEPQNLKQNCLEFQELGEYFQNALVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLVPEPQNLKQNCLEFQELGEYFQNALVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHTKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHTKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVEDTYVPKEFNAETFFHADICTLSEKQRIKKQATLALVELVHKPKAT 540
Db 481 LVNRRPCFSALEVEDTYVPKEFNAETFFHADICTLSEKQRIKKQATLALVELVHKPKAT 540
QY 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEEGKKLVAAQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEEGKKLVAAQAALGL 585
RESULT 5
AAO20111
ID AAO20111 standard; Protein; 585 AA.
AC AAO20111;
DT 06-AUG-2002 (first entry)
DE HSA protein sequence related to the growth hormone protein.
KW Serum albumin-growth hormone fusion protein; growth hormone;
KW Down's syndrome.
OS Unidentified.
PN KR99076789-A.
PD 15-OCT-1999.
PF 25-JUN-1998; 98KR-0704914.
PR 30-DEC-1995; 95GB-0026733.
PR 19-DEC-1996; 96WO-GB03164.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
DR WPI; 1997-363680/55.
DR N-PSDB; AAK99568.
XX
PT Serum albumin-growth hormone fusion protein - useful to treat growth
PT hormone related diseases, e.g. Down's syndrome
PS Disclosure; Fig 6; 21pp; Korean.
XX
CC The invention relates to a serum albumin-growth hormone fusion protein -
CC useful to treat growth hormone related diseases such as Down's syndrome.
CC This sequence represents a HSA protein related to the serum albumin-
CC growth hormone protein of the invention.
585 AA;
08:06

Query Match 100.0%; Score 3103; DB 18; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAVHFRKDLGSENFKALVLIATAFYLOQCPEPDEHVKLVNTEFAKTCVADESAE 60
Db 1 DAHSEVAVHFRKDLGSENFKALVLIATAFYLOQCPEPDEHVKLVNTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPRLVPRVEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPRLVPRVEV 120
QY 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASQKFGKRAFAKAWARLSORFFKAEFVSKLVDTLTK 240
Db 181 KLDELDEGKASSAKQRLKASQKFGKRAFAKAWARLSORFFKAEFVSKLVDTLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
Db 301 DLPSSLAADFVESKDVCKNTAEAKDVLGMFLYIARRHPDYSVLLRLAKYETTLTK 360
QY 361 CAADPHCEYAKVDFEFLVPEPQNLKQNCLEFQELGEYFQNALVRYTKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLVPEPQNLKQNCLEFQELGEYFQNALVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHTKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHTKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVEDTYVPKEFNAETFFHADICTLSEKQRIKKQATLALVELVHKPKAT 540
Db 481 LVNRRPCFSALEVEDTYVPKEFNAETFFHADICTLSEKQRIKKQATLALVELVHKPKAT 540
QY 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEEGKKLVAAQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKRADDKTCFAEEGKKLVAAQAALGL 585

RESULT 6
AAO20111
ID AAY84873 standard; protein; 585 AA.
AC AAY84873;
DT 08-AUG-2000 (first entry)
DE Amino acid sequence of a human albumin protein.
KW Human; albumin; ischemic state; serum protein; metal ion salt;
KW perloperative ischemia; ischemia; myocardial infarction;
KW progressive coronary artery disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note- "optionally acetylated, and claimed under
FT claim 56"
XX
PN WO200020840-A1
XX
PD 13-APR-2000.
XX
PF 01-OCT-1999; 99WO-US22905.
XX

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:22 ; Search time 29 Seconds
(without alignments)
593.531 Million cell updates/sec

Title: US-09-833-111-18
Perfect score: 3103
Sequence: 1 DAHSEVAHREKDLGLENFK.....TCFAEKGKLVAAQAALGL 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	3103	100.0	585	1 US-08-153-799-14	Sequence 14, Appl
2	3103	100.0	585	2 US-08-702-572-2	Sequence 2, Appl
3	3103	100.0	585	4 US-08-769-746-2	Sequence 2, Appl
4	3103	100.0	610	2 US-08-797-689-2	Sequence 2, Appl
5	3103	100.0	783	1 US-08-256-938-2	Sequence 2, Appl
6	3103	100.0	787	1 US-08-256-938-4	Sequence 4, Appl
7	3103	100.0	787	2 US-08-797-689-16	Sequence 16, Appl
8	3099	99.9	609	1 US-08-222-619-3	Sequence 3, Appl
9	3099	99.9	609	4 US-08-433-037-4	Sequence 4, Appl
10	3099	99.9	609	4 US-08-897-956A-2	Sequence 2, Appl
11	3099	99.9	609	5 PCT-US95-04075-3	Sequence 3, Appl
12	3095	99.7	978	4 US-08-897-956A-3	Sequence 3, Appl
13	3093	99.7	585	1 US-08-448-196A-3	Sequence 3, Appl
14	2458.5	79.2	583	2 US-08-984-176-1	Sequence 1, Appl
15	2458.5	79.2	583	1 US-08-448-196A-5	Sequence 5, Appl
16	2450.5	79.0	583	1 US-08-448-196A-4	Sequence 4, Appl
17	2432.5	78.4	583	1 US-08-448-196A-6	Sequence 6, Appl
18	2426	78.2	584	1 US-08-448-196A-7	Sequence 7, Appl
19	2389	77.0	582	1 US-08-134-638-1	Sequence 1, Appl
20	1249.5	40.3	609	1 US-08-222-619-4	Sequence 4, Appl
21	1249.5	40.3	609	5 PCT-US95-04075-4	Sequence 4, Appl
22	1206.5	38.9	590	2 US-08-377-309-2	Sequence 2, Appl
23	1206.5	38.9	590	4 US-09-186-723-2	Sequence 2, Appl
24	1206.5	38.9	590	4 US-08-505-012-5	Sequence 5, Appl
25	1206.5	38.9	590	4 US-09-186-949A-3	Sequence 3, Appl
26	1206.5	38.9	590	5 PCT-US96-00996-5	Sequence 5, Appl
27	1206.5	38.9	609	4 US-09-186-949A-2	Sequence 2, Appl

28	1164.5	37.5	579	1 US-08-448-196A-8	Sequence 8, Appl
29	1055	34.0	599	1 US-08-222-619-2	Sequence 2, Appl
30	1055	34.0	599	4 US-08-221-767-24	Sequence 24, Appl
31	1055	34.0	599	5 PCT-US95-04075-2	Sequence 2, Appl
32	926	29.8	393	2 US-08-377-309-7	Sequence 7, Appl
33	926	29.8	393	4 US-09-186-723-7	Sequence 7, Appl
34	926	29.8	393	4 US-08-505-012-10	Sequence 10, Appl
35	926	29.8	393	4 US-09-186-949A-8	Sequence 8, Appl
36	926	29.8	393	5 PCT-US96-00996-10	Sequence 10, Appl
37	777	25.0	324	4 US-08-505-012-12	Sequence 12, Appl
38	777	25.0	324	5 PCT-US96-00996-12	Sequence 12, Appl
39	777	25.0	325	2 US-08-377-309-8	Sequence 8, Appl
40	777	25.0	325	4 US-09-186-723-8	Sequence 8, Appl
41	777	25.0	325	4 US-08-505-012-11	Sequence 11, Appl
42	777	25.0	325	4 US-09-186-949A-9	Sequence 9, Appl
43	777	25.0	325	5 PCT-US96-00996-11	Sequence 11, Appl
44	747.5	24.1	590	1 US-08-448-196A-9	Sequence 9, Appl
45	684.5	22.1	389	2 US-08-377-309-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-153-799-14
; Sequence 14, Application US/08153799
; Patent No 5766883
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J
; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847975
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00650
; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775952
; FILING DATE: 29-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24864
; REFERENCE/DOCKET NUMBER: 92H832
; TELEPHONE: (908) 665 2400
; TELEFAX: (908) 771 6159
; TELEX: 219484
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 369..419
;   OTHER INFORMATION: /note= "Alternative C-termini of
;   OTHER INFORMATION: HSA(1-n)"
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..585
;   OTHER INFORMATION: /note= "Amino acid sequence of
;   OTHER INFORMATION: natural HSA"
; US-08-153-799-14

Query Match      100.0%; Score 3103; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKKLYEIAIRRHYPFYAPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKLYEIAIRRHYPFYAPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Qy 181 KLDELDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFAEVSCLVTLDTLK 240
Db 181 KLDELDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFAEVSCLVTLDTLK 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEFLKPLVEEPQNLKQNCSELFQGLGYKFNALLVRYTKKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLKPLVEEPQNLKQNCSELFQGLGYKFNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHKKPAT 540
Db 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHKKPAT 540

; ..

RESULT 2
US-08-702-572-2
; Sequence 2, Application US/08702572
; Patent No. 5965386
; GENERAL INFORMATION:
; APPLICANT: Kerry-Williams, Sean M
; APPLICANT: Gilbert, Sarah C
; TITLE OF INVENTION: Yeast Strains and Modified Albumins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue
```

```
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08702,572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Biswas
; REGISTRATION NUMBER: 38,384
; REFERENCE/DOCKET NUMBER: CE0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4294
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-572-2
```

```
Query Match      100.0%; Score 3103; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADSEAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKKLYEIAIRRHYPFYAPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKLYEIAIRRHYPFYAPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Qy 181 KLDELDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFAEVSCLVTLDTLK 240
Db 181 KLDELDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPFAEVSCLVTLDTLK 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEFLKPLVEEPQNLKQNCSELFQGLGYKFNALLVRYTKKVPQVST 420
Db 361 CAADPHCEYAKVDFEFLKPLVEEPQNLKQNCSELFQGLGYKFNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPKAKRMPCAEYLSVWLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHKKPAT 540
Db 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVLYVKKHKKPAT 540
```

Qy 541 KEQLKAVMDPFAAFVEKCKADDDKTCFAEBGKGLVAASQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKADDDKTCFAEBGKGLVAASQAALGL 585

RESULT 3

US-08-769-746-2
: Sequence 2, Application US/08769746
: Patent No. 6274305
: GENERAL INFORMATION:
: APPLICANT: Sonenschein, Carlos
: APPLICANT: Soto, Ana M.
: TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Medlen & Carroll, LLP
: STREET: 220 Montgomery Street, Suite 2200
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/769,746
: FILING DATE: 19-DEC-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Carroll, Peter G.
: REGISTRATION NUMBER: 32,837
: REFERENCE/DOCKET NUMBER: MBRI-02584
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 585 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-769-746-2

Query Match 100.0%; Score 3103; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.6e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKEVAHREFKDLGEENFKALVLIATAQYLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60
Db 1 DAHKEVAHREFKDLGEENFKALVLIATAQYLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPNECFLOKHKDDNPNLRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPNECFLOKHKDDNPNLRLVRPEV 120
Qy 121 DVMCTAFHDNETFLKYLXIEIARRHPYFYAPPELLFTAKRYKAATECCQAADKAACLLP 180
Db 121 DVMCTAFHDNETFLKYLXIEIARRHPYFYAPPELLFTAKRYKAATECCQAADKAACLLP 180
Qy 181 KLDELDRGKASSAKORLKASLOKFGERAFKANAVARLSORFPAEVAESKLVTDLT 240
Db 181 KLDELDRGKASSAKORLKASLOKFGERAFKANAVARLSORFPAEVAESKLVTDLT 240
Qy 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAAKADVFGLGFLYFYARRHPDYSVVLLRLAKTYETTLK 360
Db 301 DLPSLAADFVESKDVCKNYAAKADVFGLGFLYFYARRHPDYSVVLLRLAKTYETTLK 360

Qy 361 CAAADPHCYAKVDFEFKPLVEEPQNLKONCELFQELGKEYKFQNALLVRYTKKVPQVST 420
Db 361 CAAADPHCYAKVDFEFKPLVEEPQNLKONCELFQELGKEYKFQNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRLNGKVGSKCKKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRLNGKVGSKCKKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKROIKKOTALVELVHKPKAT 540
Db 481 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKROIKKOTALVELVHKPKAT 540
Qy 541 KEQLKAVMDPFAAFVEKCKADDDKTCFAEBGKGLVAASQAALGL 585
Db 541 KEQLKAVMDPFAAFVEKCKADDDKTCFAEBGKGLVAASQAALGL 585

RESULT 4

US-08-797-689-2
: Sequence 2, Application US/08797689
: Patent No. 5876969
: GENERAL INFORMATION:
: APPLICANT: Fleer, Reinhard
: APPLICANT: Fournier, Alain
: APPLICANT: Guitton, Jean-Dominique
: APPLICANT: Jung, Gerard
: APPLICANT: Yeh, Patrice
: TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
: TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rhone-Poulenc Rorer Inc.
: STREET: 500 Arcola Road, 3C43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
: ZIP: 19426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Macintosh
: OPERATING SYSTEM: System 7.1
: SOFTWARE: Word 5.1 (Patentin)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/797,689
: FILING DATE: 31-JAN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/256,927
: FILING DATE: 28-JUL-1994
: APPLICATION NUMBER: FR 92/01064
: FILING DATE: 31-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR93/00085
: FILING DATE: 28-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith Ph.D., Julie K.
: REGISTRATION NUMBER: P-38,619
: REFERENCE/DOCKET NUMBER: ST92006-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 454-3839
: TELEFAX: (610) 454-3808
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-797-689-2

Query Match 100.0%; Score 3103; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 7e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFKDLGKDFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHSEVAHFKDLGKDFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 144
QY 121 DVMTAFHNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLTP 180
DB 145 DVMTAFHNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLTP 204
QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 205 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEYENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEYENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLLRKAKTYTTLEK 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLLRKAKTYTTLEK 384
QY 361 CAADPHECYAKVDFEFPKPLVEBPQNLKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 385 CAADPHECYAKVDFEFPKPLVEBPQNLKONCELFQOLGEYKFQNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRLNKGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
DB 445 PTLVEVSRLNKGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 504
QY 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 505 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKOTALVELVKKHPKAT 564
QY 541 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 565 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 609

RESULT 5
US-08-256-938-2
; Sequence 2, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne

REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: ST92007-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-938-2

Query Match 100.0%; Score 3103; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 1e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFKDLGKDFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHSEVAHFKDLGKDFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 144
QY 121 DVMTAFHNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLTP 180
DB 145 DVMTAFHNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLTP 204
QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 205 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEYENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEYENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLLRKAKTYTTLEK 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHHPDYSVLLLRKAKTYTTLEK 384
QY 361 CAADPHECYAKVDFEFPKPLVEBPQNLKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 385 CAADPHECYAKVDFEFPKPLVEBPQNLKONCELFQOLGEYKFQNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRLNKGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 480
DB 445 PTLVEVSRLNKGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTES 504
QY 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 505 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKOTALVELVKKHPKAT 564
QY 541 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 565 KEOLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 609

RESULT 6
US-08-256-938-4
; Sequence 4, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA

```
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-256-938-4

Query Match 100.0%; Score 3103; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 1e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRLDGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 203 DAHSEVAHFRLDGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 262
QY 61 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPEV 120
Db 263 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPEV 322
QY 121 DVMTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 323 DVMTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 382
QY 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
Db 383 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 442
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
Db 443 VHTCCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 502
QY 301 DLPSLAADFVSKDCKYKAEADKDFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEK 360
Db 503 DLPSLAADFVSKDCKYKAEADKDFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEK 562
QY 361 CAADPHCEKAKVDFEKLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKKVPQVST 420
Db 563 CAADPHCEKAKVDFEKLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKKVPQVST 622
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEADYLSVLNQLCVLHEKTPVSDRVTCKCTES 480
Db 623 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEADYLSVLNQLCVLHEKTPVSDRVTCKCTES 682
QY 481 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQATLVELVKKHFKAT 540
Db 683 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQATLVELVKKHFKAT 742
QY 541 KEQLKAVMDDFAAFEVCKCKADKDKETCFAEKGKLVAAASQAALGL 585
Db 743 KEQLKAVMDDFAAFEVCKCKADKDKETCFAEKGKLVAAASQAALGL 787

; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-256-938-4

Query Match 100.0%; Score 3103; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 1e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRLDGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 203 DAHSEVAHFRLDGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 262
QY 61 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPEV 120
Db 263 NCKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPEV 322
QY 121 DVMTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 323 DVMTAFHDNEETFLKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 382
QY 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
Db 383 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 442
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
Db 443 VHTCCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 502
QY 301 DLPSLAADFVSKDCKYKAEADKDFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEK 360
Db 503 DLPSLAADFVSKDCKYKAEADKDFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEK 562
QY 361 CAADPHCEKAKVDFEKLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKKVPQVST 420
Db 563 CAADPHCEKAKVDFEKLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKKVPQVST 622
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEADYLSVLNQLCVLHEKTPVSDRVTCKCTES 480
Db 623 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEADYLSVLNQLCVLHEKTPVSDRVTCKCTES 682
QY 481 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQATLVELVKKHFKAT 540
Db 683 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQATLVELVKKHFKAT 742
QY 541 KEQLKAVMDDFAAFEVCKCKADKDKETCFAEKGKLVAAASQAALGL 585
Db 743 KEQLKAVMDDFAAFEVCKCKADKDKETCFAEKGKLVAAASQAALGL 787
```

QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCHIAEVENDEMPA 300
 DB 443 VHTCCGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCHIAEVENDEMPA 502
 QY 301 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHDPDYSVLLRLAKTYETTTLEK 360
 DB 503 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHDPDYSVLLRLAKTYETTTLEK 562
 QY 361 CAAADPHCYAKVDFEFPKPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 563 CAAADPHCYAKVDFEFPKPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 622
 QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 623 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 682
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
 DB 683 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 742
 QY 541 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEKGKLVAAASQAALGL 585
 DB 743 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEKGKLVAAASQAALGL 787

RESULT 8

US-08-222-619-3
 ; Sequence 3, Application US/08222619
 ; Patent No. 5652352
 ; GENERAL INFORMATION:
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Lyons, David
 ; APPLICANT: Wurfel, Mark
 ; APPLICANT: Wright, Samuel
 ; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Center, Patent Operations/RRC
 ; STREET: 1840 DeHavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,619
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein

US-08-222-619-3

Query Match 99.9%; Score 3099; DB 1; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.7e-286;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFDLGENFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADES 60
 DB 25 DAHSEVAHRFDLGENFKALVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADES 84
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPRLVRPEV 120

DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPRLVRPEV 144
 QY 121 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECOAADAACLLP 180
 DB 145 DVNCTAFHNEETFLKKYLYEYIARRHPYFYAPPELLFFAKRYKAAFTTECOAADAACLLP 204
 QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
 DB 205 KLDELDEGKASSAKORLKCASLQKFGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 264
 QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCHIAEVENDEMPA 300
 DB 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLECECEKPLLEKSHCHIAEVENDEMPA 324
 QY 301 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHDPDYSVLLRLAKTYETTTLEK 360
 DB 325 DPLSLAADFESKDVCKNYAEAKDVLGMLFYEARHDPDYSVLLRLAKTYETTTLEK 384
 QY 361 CAAADPHCYAKVDFEFPKPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 385 CAAADPHCYAKVDFEFPKPLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 444
 QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 445 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
 DB 505 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 564
 QY 541 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEKGKLVAAASQAALGL 585
 DB 565 KEOLKAVMDDDFAAFVEKCKCKADDKTCFAEKGKLVAAASQAALGL 609

RESULT 9

US-08-433-037-4
 ; Sequence 4, Application US/08433037
 ; Patent No. 5707828
 ; GENERAL INFORMATION:
 ; APPLICANT: Sreekrishna, Kotikanyadan
 ; APPLICANT: Barr, Kathryn A.
 ; APPLICANT: Briarley, Russell A.
 ; APPLICANT: Thill, Gregory P.
 ; APPLICANT: Tschoop, Juerg F.
 ; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,037
 ; FILING DATE: 03-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 9108Z
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-037-4

Query Match 99.9%; Score 3099; DB 1: Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 584; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 144
Qy 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK 240
Db 205 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK 264
Qy 241 VHTCCGDLLECCADDDRADLAKYICENQDSISSKLKECCCKPILLESKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECCADDDRADLAKYICENQDSISSKLKECCCKPILLESKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYAYARRHPDYSVVLLRLAKTYETTLTK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYAYARRHPDYSVVLLRLAKTYETTLTK 384
Qy 361 CAAADPHCYAKVDEFKPLVEEPQNLKQNCLEFQELGKFFQNALVRYTKVPQVST 420
Db 385 CAAADPHCYAKVDEFKPLVEEPQNLKQNCLEFQELGKFFQNALVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
Db 505 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKPKAT 564
Qy 541 KEQLKAVMDPFAAFVEKCKKADDDKTCFAEKGKLLVAASQAALGL 585
Db 565 KEQLKAVMDPFAAFVEKCKKADDDKTCFAEKGKLLVAASQAALGL 609

RESULT 10
US-08-897-956A-2
; Sequence 2, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-897-956A-2

Query Match 99.9%; Score 3099; DB 4: Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATAFYAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLRVREPV 144
Qy 121 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
Qy 181 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK 240
Db 205 KLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK 264
Qy 241 VHTCCGDLLECCADDDRADLAKYICENQDSISSKLKECCCKPILLESKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECCADDDRADLAKYICENQDSISSKLKECCCKPILLESKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYAYARRHPDYSVVLLRLAKTYETTLTK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYAYARRHPDYSVVLLRLAKTYETTLTK 384
Qy 361 CAAADPHCYAKVDEFKPLVEEPQNLKQNCLEFQELGKFFQNALVRYTKVPQVST 420
Db 385 CAAADPHCYAKVDEFKPLVEEPQNLKQNCLEFQELGKFFQNALVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHKTTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKPKAT 540
Db 505 LVNRRPCFSALEVDVETVYVPEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKPKAT 564
Qy 541 KEQLKAVMDPFAAFVEKCKKADDDKTCFAEKGKLLVAASQAALGL 585
Db 565 KEQLKAVMDPFAAFVEKCKKADDDKTCFAEKGKLLVAASQAALGL 609

RESULT 11
PCT-US95-04075-3
; Sequence 3, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRR
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US95-04075-3

Query Match 99.9%; Score 3099; DB 5; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFRKDLGENFKALVLIAPAYLOQCPEFDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHKSEVAHFRKDLGENFKALVLIAPAYLOQCPEFDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 145 DVNCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
QY 181 KLDELDEGKASSAKQRLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 205 KLDELDEGKASSAKQRLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 264
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKP LLEKSHCIAEYENDEMPA 300
DB 265 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKP LLEKSHCIAEYENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLAKTYETTTLEK 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLAKTYETTTLEK 384
QY 361 CAADPHCEYAKVDFDEKPLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 420
DB 385 CAADPHCEYAKVDFDEKPLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRFCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 505 LVNRRFCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 564
QY 541 KEOLKAVMDFFAAFEVKCKCKADDKETCFABEGKKLVAAASQAALGL 585
DB 565 KEOLKAVMDFFAAFEVKCKCKADDKETCFABEGKKLVAAASQAALGL 609

RESULT 12
US-08-897-956A-3
; Sequence 3, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR FILING DATE: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide

US-08-897-956A-3

Query Match 99.7%; Score 3095; DB 4; Length 978;
Best Local Similarity 99.8%; Pred. No. 8.1e-286;
Matches 583; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFRKDLGENFKALVLIAPAYLOQCPEFDHVKLVNEVTEFAKTCVADESAE 60
DB 212 DAHKSEVAHFRKDLGENFKALVLIAPAYLOQCPEFDHVKLVNEVTEFAKTCVADESAE 271
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 272 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 331
QY 121 DVNCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 332 DVNCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 391
QY 181 KLDELDEGKASSAKQRLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 392 KLDELDEGKASSAKQRLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 451
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKP LLEKSHCIAEYENDEMPA 300
DB 452 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCCKP LLEKSHCIAEYENDEMPA 511
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLAKTYETTTLEK 360
DB 512 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLAKTYETTTLEK 571
QY 361 CAADPHCEYAKVDFDEKPLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 420
DB 572 CAADPHCEYAKVDFDEKPLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 631
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 632 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 691
QY 481 LVNRRFCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 692 LVNRRFCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 751
QY 541 KEOLKAVMDFFAAFEVKCKCKADDKETCFABEGKKLVAAASQAALGL 584
DB 752 KEOLKAVMDFFAAFEVKCKCKADDKETCFABEGKKLVAAASQAALGL 795

RESULT 13
US-08-448-196A-3
; Sequence 3, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: BROAD JR., ROBERT L.
 REGISTRATION NUMBER: 18,757
 REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 205-544-0021
 TELEFAX: 205-544-0258
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-448-196A-3

Query Match 99.7%; Score 3093; DB 1; Length 585;
 Best Local Similarity 99.7%; Pred. No. 5.9e-286;
 Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120

QY 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 DB 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

QY 181 KLDELDEGKASSAKORLKASLQKGFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
 DB 181 KLDELDEGKASSAKORLKASLQKGFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

QY 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDMPA 300
 DB 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDMPA 300

QY 301 DLPSLAADFVESKDYCKNYAEAKDVLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360
 DB 301 DLPSLAADFVESKDYCKNYAEAKDVLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360

QY 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKQGEYKFNALLVRYTKVPQVST 420
 DB 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKQGEYKFNALLVRYTKVPQVST 420

QY 421 PTLVEVSRNLKGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLKGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

QY 481 LVNRRPCFSALEVDYTPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540
 DB 481 LVNRRPCFSALEVDYTPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540

QY 541 KQQLKAVMDPFAAFVEKCKCKADDDKTCFAEKGKLVVAASQAALGL 585
 DB 541 KQQLKAVMDPFAAFVEKCKCKADDDKTCFAEKGKLVVAASQAALGL 585

RESULT 14
 US-08-984-176-1
 Sequence 1, Application US/08984176
 Patent No. 5948609
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C
 APPLICANT: HO, JOSEPH X
 APPLICANT: RUKER, FLORIAN
 TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
 TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REFERENCE: 08/984,176
 CURRENT APPLICATION NUMBER: US/08/984,176
 CURRENT FILING DATE: 1997-12-03
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 585
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-984-176-1

Query Match 99.7%; Score 3093; DB 2; Length 585;
 Best Local Similarity 99.7%; Pred. No. 5.9e-286;
 Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHKSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120

QY 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 DB 121 DVNCTAFHDNEETFLKYLIEYIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

QY 181 KLDELDEGKASSAKORLKASLQKGFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
 DB 181 KLDELDEGKASSAKORLKASLQKGFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

QY 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDMPA 300
 DB 241 VHTCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDMPA 300

QY 301 DLPSLAADFVESKDYCKNYAEAKDVLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360
 DB 301 DLPSLAADFVESKDYCKNYAEAKDVLGMFLYIYARRHPDYSVVLLRLAKTYETTLK 360

QY 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKQGEYKFNALLVRYTKVPQVST 420
 DB 361 CAADPHCEYAKVDFEPLVEEPONLIKQNCLEFQKQGEYKFNALLVRYTKVPQVST 420

QY 421 PTLVEVSRNLKGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLKGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

QY 481 LVNRRPCFSALEVDYTPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540
 DB 481 LVNRRPCFSALEVDYTPKEFNAETFTFHADICTLSEKEROIKKQATALVELVKKPKAT 540

QY 541 KQQLKAVMDPFAAFVEKCKCKADDDKTCFAEKGKLVVAASQAALGL 585
 DB 541 KQQLKAVMDPFAAFVEKCKCKADDDKTCFAEKGKLVVAASQAALGL 585

RESULT 15
 US-08-448-196A-5
 Sequence 5, Application US/08448196A
 Patent No. 5780594
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C.
 TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
 TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
 TITLE OF INVENTION: RELATED PROTEINS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NASA
 STREET: MARSHALL SPACE FLIGHT CENTER
 CITY: HUNTSVILLE
 STATE: ALABAMA
 COUNTRY: USA
 ZIP: 35812

Job time : 35 secs

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/WFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-448-196A-5

Query Match 79.2%; Score 2458.5; DB 1; Length 583;
Best Local Similarity 75.8%; Pred. No. 1.5e-225;
Matches 442; Conservative 70; Mismatches 70; Indels 1; Gaps 1;

QY 1 DAHSEVAHREFKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADSAE 60
DB 1 DTHSETAHRENDLGEKHEKGLVIVAFSOLQOCFFEDHVKLVNEVTEFAKCAADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 119
QY 121 DVMCTAFHNEETFLKKLYEIARRHRYFYAPPELLFFAKRYKAAFTCCQADKAACLLP 180
DB 120 DAQCAAFQEDPKFLGYLYEVARRHRYFYGPPELLFHAEEYKADFTECCPADDKLACLIP 179
QY 181 KLDELREGKASSAKQRLKASLQKGFGERAFKAWAVARLSQRPFKAEFVSKLVDTLTK 240
DB 180 KLDALKERILLSSAKERLKCSSFQNGERAVKAMSVARLSQKFPKADFAEVSKIIVDTLTK 239
QY 241 VHTCCCHGDLLECDRADLAKYICENODSISKLECKECPKPLEKSHCIAEVENDEMPA 300
DB 240 VHKCCCHGDLLECDRADLAKYICHQDSTSGKLKACCDKPLQKSHCIAEVKEDDLPS 299
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLILLAKTYETTTLEK 360
DB 300 DIPALADFAEDKEDKICXHYKDAKDVLGTLFLYESSRHPDYSVSLLLRIATKYEATLEK 359
QY 361 CAAADPHCYAKVDFEKFPLVEEPQNLKONCELFGEYKFNALLVRYTKKVPQVST 420
DB 360 CAEADPPACVYTVDFQTPLVVEEPKSLVKNCDLFEVGEYDFONALIVRYTKKAPVST 419
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVNLQCLVLEHKTPTSVDRTKCCTES 480
DB 420 PTLVEIGRTLGVKGSRCCKLPESERLPCSENHLALNRLCVLHEKTPVSEKITKCCTDS 479
QY 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKQATLVLVKHKPKAT 540
DB 480 LAERPCFSALELDEGYPVKEFAETTFHADICTLPEDEKQIKKQSALAEVLVHKHKPKAT 539
QY 541 KEOLKAVMDFAAFVEKCKADKCTCFAEKGLKVAASQAL 583
DB 540 KEOLKTVLGNFSAFVAKCCGREDKEACFAEGPKLVASSQAL 582
```

Search completed: April 24, 2003, 07:26:01

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:24:07 ; Search time 266 Seconds
(without alignments)
176.225 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHFKDLGEENFK.....TCFAEGKGLVAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	585	10	US-09-929-552-2
2	3103	100.0	585	12	US-10-153-064-5
3	3103	100.0	609	12	US-10-153-064-7
4	3103	100.0	610	9	US-10-237-687-2
5	3103	100.0	610	9	US-10-237-708-2
6	3103	100.0	610	9	US-10-237-866-2
7	3103	100.0	610	9	US-10-237-871-2
8	3103	100.0	610	10	US-09-984-186-2
9	3103	100.0	651	12	US-10-153-064-133
10	3103	100.0	652	12	US-10-153-064-132
11	3103	100.0	653	12	US-10-153-064-131
12	3103	100.0	656	12	US-10-153-064-130
13	3103	100.0	676	12	US-10-153-064-129
14	3103	100.0	676	12	US-10-153-064-127
15	3103	100.0	677	12	US-10-153-064-125
16	3103	100.0	680	12	US-10-153-064-123
17	3103	100.0	787	9	US-10-237-667-16
18	3103	100.0	787	9	US-10-237-708-16
19	3103	100.0	787	9	US-10-237-866-16

Sequence 16, Appl
Sequence 16, Appl
Sequence 26, Appl
Sequence 96, Appl
Sequence 99, Appl
Sequence 105, Appl
Sequence 90, Appl
Sequence 93, Appl
Sequence 95, Appl
Sequence 98, Appl
Sequence 104, Appl
Sequence 92, Appl
Sequence 89, Appl
Sequence 102, Appl
Sequence 101, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 7, Appl
Sequence 7, Appl

787 10 US-10-237-871-16
787 10 US-09-984-186-16
788 9 US-10-073-118-26
652 12 US-10-153-064-96
652 12 US-10-153-064-99
652 12 US-10-153-064-105
660 12 US-10-153-064-90
660 12 US-10-153-064-93
676 12 US-10-153-064-95
676 12 US-10-153-064-98
676 12 US-10-153-064-104
684 12 US-10-153-064-92
1184 12 US-10-153-064-89
668 12 US-10-153-064-102
692 12 US-10-153-064-101
608 9 US-10-165-603-24
608 9 US-10-165-603-25
604 9 US-10-045-170A-1
609 10 US-09-373-913-2
590 9 US-10-115-701A-2
590 9 US-09-940-308-2
195 9 US-10-074-956-24
241 9 US-10-074-956-27
268 9 US-10-074-956-28
393 9 US-10-115-701A-7
393 9 US-09-940-308-7

ALIGNMENTS

RESULT 1

US-09-929-552-2

; Sequence 2, Application US/09929552

; Patent No. US20020123080A1

; GENERAL INFORMATION:

; APPLICANT: Sonnenschein, Carlos

; SOTO, Ana M.

; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/929,552

; FILING DATE: 14-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/769,746

; FILING DATE: 19-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.

; REGISTRATION NUMBER: 32,837

; REFERENCE/DOCKET NUMBER: MBRI-02584

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 585 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-929-552-2

Query Match 100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
DB 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSTSSKLKCCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADRADLAKYICENQDSTSSKLKCCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPDLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLLRLLAKTYETTLEKC 360
DB 301 DLPDLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLLRLLAKTYETTLEKC 360
QY 361 CAADPHCEYAKVDFEKPVLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEKPVLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVTVVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKKPAT 540
DB 481 LVNRRPCFSALEVDVTVVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKKPAT 540
QY 541 KEOLKAVMDFFAFAVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 541 KEOLKAVMDFFAFAVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
RESULT 2
US-10-153-064-5
; Sequence 5, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064-5

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60

DB 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
DB 181 KLDELDRDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRPKAEFAEVS KLVTDLTK 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSTSSKLKCCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADRADLAKYICENQDSTSSKLKCCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPDLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLLRLLAKTYETTLEKC 360
DB 301 DLPDLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLLRLLAKTYETTLEKC 360
QY 361 CAADPHCEYAKVDFEKPVLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEKPVLVEEPQNLKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVTVVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKKPAT 540
DB 481 LVNRRPCFSALEVDVTVVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVKKHKKPAT 540
QY 541 KEOLKAVMDFFAFAVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 541 KEOLKAVMDFFAFAVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585

RESULT 3
US-10-153-064-7
; Sequence 7, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064-7

Query Match 100.0%; Score 3103; DB 12; Length 609;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
DB 25 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 144
QY 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180
DB 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAACLLP 180

Db 145 DVNCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204
QY 181 KLDELDECKASSAKORLKACSLQKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTk 240
Db 205 KLDELDECKASSAKORLKACSLQKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTk 264
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECKECPKLLKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLECKECPKLLKSHCIAEVENDEMPA 324
QY 301 DLPSSAADFVESKDVCKNYAEAKDVLGMFLYIARRHPDYVSVLNLCLVHEKTPVSDRVTCKCTES 360
Db 325 DLPSSAADFVESKDVCKNYAEAKDVLGMFLYIARRHPDYVSVLNLCLVHEKTPVSDRVTCKCTES 384
QY 361 CAADPHCEYAKVDFEFLVPEEPNLKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420
Db 385 CAADPHCEYAKVDFEFLVPEEPNLKQNCLEFQELGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRNLGVSKCKCKHPEAKRMPCAEDYLSVVLNLCLVHEKTPVSDRVTCKCTES 480
Db 445 PTLVEVSRNLGVSKCKCKHPEAKRMPCAEDYLSVVLNLCLVHEKTPVSDRVTCKCTES 504
QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQATALVELVKKHPKAT 540
Db 505 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQATALVELVKKHPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGL 585
Db 565 KEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGL 609

RESULT 4

US-10-237-667-2

; Sequence 2, Application US/10237667

; Publication No. US2003002308A1

; GENERAL INFORMATION:

; APPLICANT: Fleer, Reinhard

; Fournier, Alain

; Guitton, Jean-Dominique

; Jung, Gerard

; Yeh, Patrice

; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.1

; SOFTWARE: Word 5.1 (PatentIn)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/237,667

; FILING DATE: 10-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/797,689

; FILING DATE: 31-JAN-1997

; APPLICATION NUMBER: US 08/256,927

; FILING DATE: 28-JUL-1994

; APPLICATION NUMBER: FR 92/01064

; FILING DATE: 31-JAN-1992

; APPLICATION NUMBER: PCT/FR93/00085

; FILING DATE: 28-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith Ph.D., Julie K.

; REGISTRATION NUMBER: P-38,619

; REFERENCE/DOCKET NUMBER: ST92006-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-3839

; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 610 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-237-667-2

Query Match

Best Local Similarity 100.0%; Score 3103; DB 9; Length 610;

Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRKDLGLENFKALVLIATFAQYLOQCPPEDEHVKLVNEVTEFAKTCAVDESAE 60

Db 25 DAHKSEVAHRKDLGLENFKALVLIATFAQYLOQCPPEDEHVKLVNEVTEFAKTCAVDESAE 84

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120

Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144

QY 121 DVNCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180

Db 145 DVNCTAFHDNEETFLKKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204

QY 181 KLDELDECKASSAKORLKACSLQKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTk 240

Db 205 KLDELDECKASSAKORLKACSLQKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLTk 264

QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECKECPKLLKSHCIAEVENDEMPA 300

Db 265 VHTCCGDLLECCADRADLAKYICENQDSISSKLECKECPKLLKSHCIAEVENDEMPA 324

QY 301 DLPSSAADFVESKDVCKNYAEAKDVLGMFLYIARRHPDYVSVLNLCLVHEKTPVSDRVTCKCTES 360

Db 325 DLPSSAADFVESKDVCKNYAEAKDVLGMFLYIARRHPDYVSVLNLCLVHEKTPVSDRVTCKCTES 384

QY 361 CAADPHCEYAKVDFEFLVPEEPNLKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420

Db 385 CAADPHCEYAKVDFEFLVPEEPNLKQNCLEFQELGEYKFNALLVRYTKKVPQVST 444

QY 421 PTLVEVSRNLGVSKCKCKHPEAKRMPCAEDYLSVVLNLCLVHEKTPVSDRVTCKCTES 480

Db 445 PTLVEVSRNLGVSKCKCKHPEAKRMPCAEDYLSVVLNLCLVHEKTPVSDRVTCKCTES 504

QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQATALVELVKKHPKAT 540

Db 505 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQATALVELVKKHPKAT 564

QY 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGL 585

Db 565 KEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGL 609

RESULT 5

US-10-237-708-2

; Sequence 2, Application US/10237708

; Publication No. US20030036170A1

; GENERAL INFORMATION:

; APPLICANT: Fleer, Reinhard

; Fournier, Alain

; Guitton, Jean-Dominique

; Jung, Gerard

; Yeh, Patrice

; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-708-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFKDGLGENFKALVLIAPAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 60
DB 25 DAHKSEVAHFKDGLGENFKALVLIAPAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 145 DVNCTAFHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 204
QY 181 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPKAEFAVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPKAEFAVSKLVTDLTK 264
QY 241 VHTCCGHDLLCADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 300
DB 265 VHTCCGHDLLCADRADLAKYICENQDSISSKLEKCECKPLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVSKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETLEK 360
DB 325 DLPSLAADFVSKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETLEK 384
QY 361 CAAADPHCYAKVDFDEKPLVEEPQNLKQNCSELFQOLGEYKFQNALLYRYTKKVPQVST 420
DB 385 CAAADPHCYAKVDFDEKPLVEEPQNLKQNCSELFQOLGEYKFQNALLYRYTKKVPQVST 444
QY 421 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480

DB 445 PTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 504
QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 505 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDDKCTCFABEGKKLVAAASQAALGL 585
DB 565 KEQLKAVMDDDFAAFVEKCKCKADDDKCTCFABEGKKLVAAASQAALGL 609

RESULT 6
US-10-237-866-2
; Sequence 2, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,866
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-866-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFKDGLGENFKALVLIAPAOYLQOCPEHDHVKLVNTEFAKTCVADESAE 60

Db 25 DAHSEVAHREKDLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 144
Qy 121 DVMTAFHDNEETFLKYLKYLIEIARRHPYFYAPPELLFFAKRYKAATFECQAADKAACLLP 180
Db 145 DVMTAFHDNEETFLKYLKYLIEIARRHPYFYAPPELLFFAKRYKAATFECQAADKAACLLP 204
Qy 181 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRFPAEFAEYVSKLVTDLT 240
Db 205 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRFPAEFAEYVSKLVTDLT 264
Qy 241 VHTCCGDLLECADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEAARRHPDYVSVLLLRKAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEAARRHPDYVSVLLLRKAKTYETTLK 384
Qy 361 CAADDPHECYAKVDFEPLVEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420
Db 385 CAADDPHECYAKVDFEPLVEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDYVYPKEFNAETFTFHADICTLSEKEROIKQTALVELVHKPKAT 540
Db 505 LVNRRPCFSALEVDYVYPKEFNAETFTFHADICTLSEKEROIKQTALVELVHKPKAT 564

RESULT 7

US-10-237-871-2

; Sequence 2, Application US/10237871

; Publication No. US20030036172A1

; GENERAL INFORMATION:

; APPLICANT: Fournier, Alain

; Guitton, Jean-Dominique

; Jung, Gerard

; Yeh, Patrice

; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION

; CONTAINING SAID POLYPEPTIDES

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.1

; SOFTWARE: Word 5.1 (patentIn)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/237,871

; FILING DATE: 10-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/797,689

; FILING DATE: 31-JAN-1997

; APPLICATION NUMBER: US 08/256,927

; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: PR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-871-2

Query Match 100.0%; Score 3103; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREKDLGEENFKALVLIAPFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 144
Qy 121 DVMTAFHDNEETFLKYLKYLIEIARRHPYFYAPPELLFFAKRYKAATFECQAADKAACLLP 180
Db 145 DVMTAFHDNEETFLKYLKYLIEIARRHPYFYAPPELLFFAKRYKAATFECQAADKAACLLP 204
Qy 181 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRFPAEFAEYVSKLVTDLT 240
Db 205 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRFPAEFAEYVSKLVTDLT 264
Qy 241 VHTCCGDLLECADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVENDEMPA 300
Db 265 VHTCCGDLLECADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEAARRHPDYVSVLLLRKAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEAARRHPDYVSVLLLRKAKTYETTLK 384
Qy 361 CAADDPHECYAKVDFEPLVEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420
Db 385 CAADDPHECYAKVDFEPLVEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
Qy 481 LVNRRPCFSALEVDYVYPKEFNAETFTFHADICTLSEKEROIKQTALVELVHKPKAT 540
Db 505 LVNRRPCFSALEVDYVYPKEFNAETFTFHADICTLSEKEROIKQTALVELVHKPKAT 564
Qy 541 KEOLKAVMDFFAAVFEKCKKADDETCFAEKGKLVAAASQAALGL 585
Db 565 KEOLKAVMDFFAAVFEKCKKADDETCFAEKGKLVAAASQAALGL 609

RESULT 8

US-09-984-186-2

; Sequence 2, Application US/09984186

; Patent No. US20020151011A1

; GENERAL INFORMATION:

; APPLICANT: Fleeer, Reinhard

; Fournier, Alain

Guillon, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEROF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-984-186-2
Query Match 100.0%; Score 3103; DB 10; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAHFRKDLGENFKALVLIATAFYLOQCPEHDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHSEVAHFRKDLGENFKALVLIATAFYLOQCPEHDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 85 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 145 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 204
QY 181 KLDELDEGKASSAKORLKCASLOKFGGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKCASLOKFGGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 264
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 300
DB 265 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTLEKC 360

DB 325 DLPSSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTLEKC 384
QY 361 CAAADPHECYAKVFDEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 385 CAAADPHECYAKVFDEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 444
QY 421 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQTAFLVELVKKHKPKAT 540
DB 505 LVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQTAFLVELVKKHKPKAT 564
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 585
DB 565 KEQLKAVMDDDFAAFVEKCKCKADDDKTCFAEEGKKLVAASQAALGL 609
RESULT 9
US-10-153-064-133
; Sequence 133, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-133
Query Match 100.0%; Score 3103; DB 12; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAHFRKDLGENFKALVLIATAFYLOQCPEHDHVKLVNEVTEFAKTCVADESAE 60
DB 67 DAHSEVAHFRKDLGENFKALVLIATAFYLOQCPEHDHVKLVNEVTEFAKTCVADESAE 126
QY 61 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 127 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 186
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 187 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 246
QY 181 KLDELDEGKASSAKORLKCASLOKFGGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 247 KLDELDEGKASSAKORLKCASLOKFGGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 306
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 300
DB 307 VHTTECHGDLLECCADRADLAKYICENQDSISSKKECEKPLLEKSHCIAEVENDEMPA 366
QY 301 DLPSSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTLEKC 360
DB 367 DLPSSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLRLRAKTYETTLEKC 426
QY 361 CAAADPHECYAKVFDEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 420
DB 427 CAAADPHECYAKVFDEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKKVPQVST 486
QY 421 PTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480

Db 487 PTLVEYSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 546
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
Db 547 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 606
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
Db 607 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 651

RESULT 10
US-10-153-064-132
; Sequence 132, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-132

Query Match 100.0%; Score 3103; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFDLGEENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 60
Db 68 DAHKSEVAHRFDLGEENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 127
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 128 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 187
QY 121 DVMTAFHNEETFLKKLYEYIARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 180
Db 188 DVMTAFHNEETFLKKLYEYIARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 247
QY 181 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLT 240
Db 248 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLT 307
QY 241 VHTECCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
Db 308 VHTECCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 367
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLRAKTYETTLEK 360
Db 368 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLRAKTYETTLEK 427
QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 420
Db 428 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 487
QY 421 PTLVEYSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 488 PTLVEYSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 547
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
Db 548 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 607
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585

Db 608 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 652

RESULT 11
US-10-153-064-131
; Sequence 131, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-131

Query Match 100.0%; Score 3103; DB 12; Length 653;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFDLGEENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 60
Db 69 DAHKSEVAHRFDLGEENFKALVLI AFAQYLOQCPPEHVKLVNVEYTEFAKTCADESAE 128
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 129 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 188
QY 121 DVMTAFHNEETFLKKLYEYIARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 180
Db 189 DVMTAFHNEETFLKKLYEYIARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 248
QY 181 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLT 240
Db 249 KLDELDEGKASSAKQRLKASLOKFGERAFAKAWARLSQRFPKAEFAEVSCLVTDLT 308
QY 241 VHTECCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
Db 309 VHTECCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 368
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLRAKTYETTLEK 360
Db 369 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYFYARRHPDYSVVLRLRAKTYETTLEK 428
QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 420
Db 429 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFOLGEYKFNALLVRYTKVPQVST 488
QY 421 PTLVEYSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 489 PTLVEYSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 548
QY 481 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
Db 549 LVNRRPCFSALEVDEYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 608
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
Db 609 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 653

RESULT 12
US-10-153-064-130
; Sequence 130, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-130

Query Match 100.0%; Score 3103; DB 12; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHFRKDLGEENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 60
DB 72 DAHKSEVAHFRKDLGEENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 131
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 132 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 191
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 192 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 251
QY 181 KLDELDEGKASSAKQRLKASQKQGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 252 KLDELDEGKASSAKQRLKASQKQGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 311
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 300
DB 312 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 371
QY 301 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTTLEK 360
DB 372 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTTLEK 431
QY 361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 420
DB 432 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 491
QY 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 492 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 551
QY 481 LVNRRPCFSALEVDYETVPKEFNAETFTPHADICTLSEKERQIKKQATLALVELVKKPKAT 540
DB 552 LVNRRPCFSALEVDYETVPKEFNAETFTPHADICTLSEKERQIKKQATLALVELVKKPKAT 611
QY 541 KEQLKAVMDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAALGL 585
DB 612 KEQLKAVMDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAALGL 656

RESULT 13

US-10-153-064-127
; Sequence 127, Application US/10153064
; Patent No. US200201428141
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-127

Query Match 100.0%; Score 3103; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHFRKDLGEENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 60
DB 92 DAHKSEVAHFRKDLGEENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 151
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 152 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 211
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
DB 212 DVMTAFHDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 271
QY 181 KLDELDEGKASSAKQRLKASQKQGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 272 KLDELDEGKASSAKQRLKASQKQGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 331
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 300
DB 332 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 391
QY 301 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTTLEK 360
DB 392 DLPSLAADFVESKDVCNKYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTTLEK 451
QY 361 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 420
DB 452 CAADPHCEYAKVDFEFPKPLVEEPQNLKQNCSELFQOLGEYKFNALLVRYTKKVPQVST 511
QY 421 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 512 PTLVEVSRLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 571
QY 481 LVNRRPCFSALEVDYETVPKEFNAETFTPHADICTLSEKERQIKKQATLALVELVKKPKAT 540
DB 572 LVNRRPCFSALEVDYETVPKEFNAETFTPHADICTLSEKERQIKKQATLALVELVKKPKAT 631
QY 541 KEQLKAVMDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAALGL 585
DB 632 KEQLKAVMDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAALGL 676

RESULT 14

US-10-153-064-129
; Sequence 129, Application US/10153064
; Patent No. US200201428141
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-129

```

Query Match      100.0%; Score 3103; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVHRFKDLGEEFNKALVLIAPAYLQOCPPEDHVKLVNVEVTEFAKTCVADESAAE 60
    |
    |
    |
Db 92 DAHKSEVHRFKDLGEEFNKALVLIAPAYLQOCPPEDHVKLVNVEVTEFAKTCVADESAAE 151
    |
    |
    |
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
    |
    |
    |
Db 152 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 211
    |
    |
    |
Qy 121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
    |
    |
    |
Db 212 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 271
    |
    |
    |
Qy 181 KLDELDRSGKASSAKORLKCSLQFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
    |
    |
    |
Db 272 KLDELDRSGKASSAKORLKCSLQFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 331
    |
    |
    |
Qy 241 VHTTECHGDLLECADDRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 300
    |
    |
    |
Db 332 VHTTECHGDLLECADDRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 391
    |
    |
    |
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 360
    |
    |
    |
Db 392 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 451
    |
    |
    |
Qy 361 CAADPHCEYAKVDFEFPKPLVEEPONLIKQNCLEFEQLGEYKFQNALVRYTKVPQVST 420
    |
    |
    |
Db 452 CAADPHCEYAKVDFEFPKPLVEEPONLIKQNCLEFEQLGEYKFQNALVRYTKVPQVST 511
    |
    |
    |
Qy 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 480
    |
    |
    |
Db 512 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 571
    |
    |
    |
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 540
    |
    |
    |
Db 572 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 631
    |
    |
    |
Qy 541 KEQLKAVMDDFAAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
    |
    |
    |
Db 632 KEQLKAVMDDFAAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 676

RESULT 15
US-10-153-064-125
; Sequence 125, Application US/10153064
; Patent No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-064-125

```

```

Query Match      100.0%; Score 3103; DB 12; Length 677;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVHRFKDLGEEFNKALVLIAPAYLQOCPPEDHVKLVNVEVTEFAKTCVADESAAE 60
    |
    |
    |
Db 93 DAHKSEVHRFKDLGEEFNKALVLIAPAYLQOCPPEDHVKLVNVEVTEFAKTCVADESAAE 152
    |
    |
    |

```

```

Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 120
    |
    |
    |
Db 153 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPRLVRPEV 212
    |
    |
    |
Qy 121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
    |
    |
    |
Db 213 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 272
    |
    |
    |
Qy 181 KLDELDRSGKASSAKORLKCSLQFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
    |
    |
    |
Db 273 KLDELDRSGKASSAKORLKCSLQFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 332
    |
    |
    |
Qy 241 VHTTECHGDLLECADDRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 300
    |
    |
    |
Db 333 VHTTECHGDLLECADDRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 392
    |
    |
    |
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 360
    |
    |
    |
Db 393 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 452
    |
    |
    |
Qy 361 CAADPHCEYAKVDFEFPKPLVEEPONLIKQNCLEFEQLGEYKFQNALVRYTKVPQVST 420
    |
    |
    |
Db 453 CAADPHCEYAKVDFEFPKPLVEEPONLIKQNCLEFEQLGEYKFQNALVRYTKVPQVST 512
    |
    |
    |
Qy 421 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 480
    |
    |
    |
Db 513 PTLVEVSRNLKGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHBEKTPVSDRVTKCCTES 572
    |
    |
    |
Qy 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 540
    |
    |
    |
Db 573 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKHKPKAT 632
    |
    |
    |
Qy 541 KEQLKAVMDDFAAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
    |
    |
    |
Db 633 KEQLKAVMDDFAAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 677

```

Search completed: April 24, 2003, 07:41:08
Job time : 267 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 21 Seconds
(without alignments)
2678.030 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHRFKDLGEENFK.....TCFAEGKGLVAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3103	100.0	609	1 ABHUS	serum albumin prec
2	2942	94.8	609	2 A47391	serum albumin prec
3	2820	84.4	608	2 S57632	serum albumin prec
4	2475.5	79.8	607	1 ABHOS	serum albumin prec
5	2446.5	78.8	607	1 ABHOS	serum albumin prec
6	2432.5	78.4	607	1 ABHOS	serum albumin prec
7	2426	78.2	608	1 ABHOS	serum albumin prec
8	2411.5	77.7	605	1 ABPGS	serum albumin prec
9	2387	76.9	609	2 JC5838	albumin - Mongolia
10	1861	60.0	453	2 A05139	serum albumin - mo
11	1557.5	50.2	615	1 ABCHS	serum albumin prec
12	1253.5	40.4	609	2 JC4258	alpha-fetoprotein
13	1249.5	40.3	609	1 FEHU	alpha-fetoprotein
14	1242.5	40.0	609	1 FPGO	alpha-fetoprotein
15	1205	38.8	607	1 ABXL72	74K albumin prec
16	1181.5	38.1	265	2 I46986	albumin - dog (fra
17	1175.5	37.9	608	1 ABXL68	68K serum albumin
18	1084	34.9	605	1 FPM5	alpha-fetoprotein
19	1067	34.4	611	1 FPRT	alpha-fetoprotein
20	1055	34.0	599	1 A54906	afamin precursor -
21	928.5	29.9	614	2 S99517	serum albumin prec
22	928	29.9	608	2 A53195	afamin precursor -
23	747.5	24.1	608	1 ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1 ABONS2	serum albumin 2 pr
25	699	22.5	382	2 A37253	serum albumin - bu
26	440.5	14.2	1423	1 S27941	serum albumin - se
27	386	12.4	474	1 VYHUI	vitamin D-binding
28	385	12.4	476	1 VYRTD	vitamin D-binding
29	372	12.0	472	1 A35327	vitamin D-binding

ALIGNMENTS

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

N:Contains: kinetensin

C:Species: Homo sapiens (man)

C:Date: 29-Jul-1981 #sequence_revision 31-Jan-1997 #text_change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Goulty, C.M.; Najarian, R.C.; See

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia c

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, 'K', 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J000078; GB:L00132; GB:L00133; NID:g28591; PIDN:CA

R:Dugaiczyk, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, 'G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions a

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <URA>

A:Cross-references: GB:M13075; NID:g178330; PIDN:AAA51688.1; PID:g553173

R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBDJ

A:Residues: 282-290, 'KSRFDLQ', <WAT>

A:Cross-references: GB:S69192; NID:g546032; PIDN:AAB30282.1; PID:g546033

A>Note: This frame-shift variant, designated albumin Roma, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putna

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRRVKNLLQVKLP', <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

cag island protein
cag pathogenicity
calcium-binding pr
hypothetical prote
major surface glyco
cell surface glyco
hypothetical prote
hypothetical specifi
sperm tail-specifi
kinesin homolog p2
major surface glyco
myosin heavy chain
cell-cycle-depende
glycoprotein A - p
hypothetical prote
giantin - human
embryonic muscle m

A:Note: this frame-shift variant is designated albumin Bazzano; four additional variants
R:Menaya, J.; Parrilla, R.; Ayuso, M.S.
submitted to the EMBL Data Library, March 1995
A:Reference number: G08292
A:Accession: G01747
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-120, 'G', 122-455 <MEN>
A:Cross-references: EMBL:U22961; NID:G763428; PIDN:AAA64922.1; PID:G763431
R:Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A:Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*
A:Reference number: S55314; MUID:95275251; PMID:7755581
A:Accession: S55314
A:Molecule type: protein
A:Residues: 19-27 <LED>
R:Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A:Title: Complete amino acid sequence of human serum albumin.
A:Reference number: A91420; MUID:76187907; PMID:1225573
A:Accession: A91420
A:Molecule type: protein
A:Residues: 23-117, 'EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-
R:Roehr, U.; Spittelier, G.; Tripter, D.
Justus Liebig's Ann. Chem. 9, 881-884, 1988
A:Title: Isolation and structure elucidation of middle-molecular weight peptides from u
A:Reference number: S06422
A:Note: this paper is in German, with an English abstract
A:Accession: S06422
A:Molecule type: protein
A:Residues: 25-48 <ROE>
R:Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A:Title: Mass spectrometric identification of modifications to human serum albumin treat
A:Reference number: S36882; MUID:93384321; PMID:8373198
A:Accession: S36882
A:Molecule type: protein
A:Residues: 45-67; 141-160; 311-337; 469-490; 570-581 <FIN>
R:Kausler, E.; Spittelier, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A:Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
A:Reference number: S17599; MUID:92126241; PMID:1772598
A:Accession: S17599
A:Molecule type: protein
A:Residues: 25-54; 354-357; 431-447 <KAU>
A:Note: 49-Leu was also found
R:Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: A45800
A:Molecule type: protein
A:Residues: 166-173 <CAR>
R:Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A:Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A:Reference number: A03239; MUID:86242180; PMID:3087352
A:Accession: A03239
A:Molecule type: protein
A:Residues: 166-173, 'L' <MOG>
R:Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madisson, J.; Watkins, S
Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A:Title: Mutations in genetic variants of human serum albumin found in Italy.
A:Reference number: A38255; MUID:91062352; PMID:2247440
A:Accession: C38255
A:Molecule type: protein
A:Residues: 76-111 <GAL>
A:Accession: B38255
A:Molecule type: protein
A:Residues: 82-105, 'K', 107-110 <GAL2>
A:Note: this variant is designated albumin Vibo Valentia
A:Accession: A38255
A:Molecule type: protein

A:Residues: 76-83, 'K', 85-106 <GAL3>
A:Note: this variant is designated albumin Torino
R:Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A:Title: The structural characterization and bilirubin-binding properties of albumin
A:Reference number: S33298; MUID:93292504; PMID:8513793
A:Accession: S33298
A:Molecule type: protein
A:Residues: 255-263, 'E', 265-281 <MIN1>
A:Note: this variant is designated albumin Herborn
R:Minchiotti, L.; Galliano, M.; Stopini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por
Biochim. Biophys. Acta 1119, 232-238, 1992
A:Title: Two albumins with identical electrophoretic mobility are produced by dif
A:Reference number: S21078; MUID:92190239; PMID:1347703
A:Accession: S21078
A:Molecule type: protein
A:Residues: 354-356, 'K', 358-378 <MIN2>
A:Note: this variant is designated albumin Sondrio; another variant Paris-2 is report
R:He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A:Title: Atomic structure and chemistry of human serum albumin.
A:Reference number: A46756; MUID:92334427; PMID:1630489
A:Contents: annotation; X-ray crystallography, 2.8 angstroms
R:Brown, J.R.; Shockley, P.; Behrens, P.Q.
In The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-
A:Reference number: A9442
A:Contents: annotation; three-dimensional structure and disulfide bonds
R:Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A:Title: Disulfide bonds in human serum albumin.
A:Reference number: A90930
A:Contents: annotation; disulfide bonds
R:Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A:Title: Lysine residue 240 of human serum albumin is involved in high-affinity bindi
A:Reference number: A90299; MUID:78186630; PMID:656055
A:Contents: annotation; bilirubin-binding site
R:Petters, T.; Reed, R.G.
In Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjöholm, I., eds., 11-
A:Title: Serum albumin: conformation and active sites.
A:Reference number: A94408
A:Contents: annotation; binding sites
R:Harper, M.E.; Dugaiczky, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A:Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein ge
A:Reference number: A90028; MUID:83279982; PMID:6192711
A:Contents: annotation; gene position
R:Walker, J.E.
FEBS Lett. 66, 173-175, 1976
A:Title: Lysine residue 199 of human serum albumin is modified by acetylsalicylic ac
A:Reference number: A46755; MUID:76257808; PMID:955075
A:Contents: annotation
A:Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicylic a
R:Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C.
FEBS Lett. 298, 266-268, 1992
A:Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phos
A:Reference number: A56294; MUID:92183881; PMID:1544460
A:Contents: annotation
A:Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; 1
atase activity
C:Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesiz
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (we
C:Comment: A large number of variants of human serum albumin have been described.
C:Genetics:
A:Gene: GDB:ALB
A:Cross-references: GDB:118990; OMIM:103600
A:Map position: 4q11-q13
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyri
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-609/Product: serum albumin #status experimental <MPT>
F:29-202/Domain: serum albumin repeat homology <SAL>

F:166-174/Product: kinetensin #status experimental <KIP>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA2>
F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,413-592/Binding site: copper (His) #status predicted
F:214/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 100.0%; Score 3103; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 7,4e-198;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRKDLGEENFKALVLIATAFYQYLOQCFFEDHVKLVNVTFAKTCVADESAB 60
|||||
DB 25 DAHKSEVAHRKDLGEENFKALVLIATAFYQYLOQCFFEDHVKLVNVTFAKTCVADESAB 84
|||||

QY 61 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
|||||
DB 85 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 144
|||||

QY 121 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
|||||
DB 145 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 204
|||||

QY 181 KLDELDRDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLT 240
|||||
DB 205 KLDELDRDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLT 264
|||||

QY 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
|||||
DB 265 VHTCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
|||||

QY 301 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 360
|||||
DB 325 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 384
|||||

QY 361 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKVPQVST 420
|||||
DB 385 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKVPQVST 444
|||||

QY 421 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVNLQVLHKTVPDSRVTKCCTES 480
|||||
DB 445 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVNLQVLHKTVPDSRVTKCCTES 504
|||||

QY 481 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQALVELVKKHPRAT 540
|||||
DB 505 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQALVELVKKHPRAT 564
|||||

QY 541 KEQLKAVMDDFAAFEVCKCKADKDKETCFPAEKGKLVVAASQAALGL 585
|||||
DB 565 KEQLKAVMDDFAAFEVCKCKADKDKETCFPAEKGKLVVAASQAALGL 609
|||||

RESULT 2
A47391
serum albumin precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C:Accession: A47391
R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A:Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilirubin binding site
A:Reference number: A47391; MUID:93211971; PMID:8460152
A:Contents: B/B homozygote
A:Accession: A47391
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-600 <WAT>
A:Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIIP:128281)
C:Superfamily: serum albumin; serum albumin repeat homology
F:21-194/Domain: serum albumin repeat homology <SA1>
F:213-386/Domain: serum albumin repeat homology <SA2>

F:405-584/Domain: serum albumin repeat homology <SA3>
Query Match 94.8%; Score 2942; DB 2; Length 600;
Best Local Similarity 93.5%; Pred. No. 3.3e-187;
Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRKDLGEENFKALVLIATAFYQYLOQCFFEDHVKLVNVTFAKTCVADESAB 60
|||||
DB 17 DTHKSEVAHRKDLGEENFKGLVAVAFSOLQCCPFEEHVKLVNVTFAKTCVADESAB 76
|||||

QY 61 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
|||||
DB 77 NCDKSLHLTFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 136
|||||

QY 121 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
|||||
DB 137 DVMTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 196
|||||

QY 181 KLDELDRDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLT 240
|||||
DB 197 KLDELDRDEGKASSAKQRLKASLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLT 256
|||||

QY 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
|||||
DB 257 VHTCCHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 316
|||||

QY 301 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 360
|||||
DB 317 DLPSLAADFEVSKDCKNYAEAKDVLGMFLYFYARRHPDYSVLLLRLLAKTYETTLK 376
|||||

QY 361 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKVPQVST 420
|||||
DB 377 CAADPHCYAKVDFEPLVEEPQNLKQNCLEFEQGEYKFNALLVRYTKVPQVST 436
|||||

QY 421 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVNLQVLHKTVPDSRVTKCCTES 480
|||||
DB 437 PTLVSVNLGKVGSKCKHPEAKRMPCAEDYLSVNLQVLHKTVPDSRVTKCCTES 496
|||||

QY 481 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQALVELVKKHPRAT 540
|||||
DB 497 LVNRRPCFSALVEVDYTPKFEKNAETFTFHADICTLSEKEROIKKQALVELVKKHPRAT 556
|||||

QY 541 KEQLKAVMDDFAAFEVCKCKADKDKETCFPAEKGKLVVAASQAAL 583
|||||
DB 557 KEQLKAVMDDFAAFEVCKCKADKDKETCFPAEKGKLVVAASQAAL 599
|||||

RESULT 3
S57632
serum albumin precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
C:Accession: J04660; S57632
R:Hilger, C.; Grigioni, F.; Hentges, F.
Gene 169, 295-296, 1996
A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A:Reference number: J04660; MUID:96194824; PMID:8647469
A:Accession: J04660
A:Molecule type: mRNA
A:Residues: 1-608 <HI2>
A:Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
A:Experimental source: liver
C:Comment: This protein is the major protein component in plasma. It functions as a
ein has 35 conserved cysteine residues.
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: liver; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRP>
F:25-608/Product: serum albumin #status predicted <MAT>
F:229-202/Domain: serum albumin repeat homology <SA1>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA3>

A;Residues: 1-32 <MAG>
R;Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Electrophoretic transfer filter from an analytical isoelectrofocusing gel
A;Reference number: A60808; MUID:88267456; PMID:3389500
A;Accession: B60808
A;Molecule type: protein
A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10780
A;Molecule type: protein
A;Residues: 25-41, 'H', '43-57, 59-64 <STR>
R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteases
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: A45800
A;Molecule type: protein
A;Residues: 163-172 <CAR>
R;Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from pe
A;Reference number: A26693; MUID:87194805; PMID:2437111
A;Accession: A26693
A;Molecule type: protein
A;Residues: 165-172, 'L', 'CA2>
R;Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A;Title: Sequence of residues 400-403 of bovine serum albumin.
A;Reference number: A90309; MUID:82023364; PMID:7283978
A;Accession: A90309
A;Molecule type: protein
A;Residues: 402-433 <REE>
R;Brown, J.R.
Fed. Proc. 34, 591, 1975
A;Title: Structure of bovine serum albumin.
A;Reference number: A91458
A;Accession: A91458
A;Molecule type: protein
A;Residues: 25-41, 'H', '43-117, 'EQ', 120-179, 181-189, 'E', 191-194, 'A', 196-213, 'T', 215-288, 'H'
R;Brown, J.R.
submitted to the Atlas, April 1975
A;Reference number: A94551
A;Accession: A94551
A;Molecule type: protein
A;Residues: 190-195 <BR2>
R;Brown, J.R.
Fed. Proc. 33, 1389, 1974
A;Reference number: A91457
A;Contents: annotation; disulfide bonds
R;Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A;Title: Preparation and characterization of novel substrates of insulin proteinase (EC
A;Reference number: S55232; MUID:95031935; PMID:7945219
A;Accession: S55232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 529-536;569-572 <WER>
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; copper binding; duplication; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-607/Product: serum albumin #status experimental <MP>
F;29-201/Domain: serum albumin repeat homology <SAL>
F;412-591/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-392, 4

Query Match

78.8%; Score 2446.5; DB 1; Length 607;

Best Local Similarity 75.6%; Pred. No. 2.1e-154;
Matches 441; Conservative 71; Mismatches 70; Indels 1; Gaps 1;
QY 1 DAUKSEVAHFRKDLGEENFKALVIAFAQYLOQCFFDHVKLVNEVTEFAKTCVADSEAE 60
DB 25 DTHKSEIAHFRKDLGEOQFKGLVIAFSQYLOQCFFDHVKLVNELTEFAKTCVADSEHA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPLRVPEY 120
DB 85 GCEKSLHTLFGDELCKVASLRETYGDMADCCOEPERNECFLOSHKDDSPDLPLK-KPDP 143
QY 121 DVMCTAPHDNEETFLKYLIEIARRHPYFYAPPELLFAKRYKAAFTCCQAADKAACLLP 180
DB 144 NTLCDDEFKADKKFKWGLYIEIARRHPYFYAPPELLYANKYNGVFOCCQAEDRGACLLP 203
QY 181 KLDELDEGRKASSAKORLKCAQKQFGERAFKAWARLQRRPKAEFAEVSKLVTDLTK 240
DB 204 KETMRKRVLIASSARQRLRCASQKQFGERALKAWARLQRRPKAEFAEVSKLVTDLTK 263
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCKPLLEKSHCIAEVENDEMPA 300
DB 264 VHKCCCHGDLLECADRADLAKYICDNQDTISSKLECCCKPLLEKSHCIAEVEKDAIPE 323
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGFMFLYIARRHPDYSVLLRLAKTYETTLK 360
DB 324 NLPLPLTADFAEDKDYCKNYQEAQDAFLGSLFYIARRHPDYSVLLRLAKTYETTLK 383
QY 361 CAADPHCEYAKVDFEPKPLVEEPQNLKONCELFEOGLGEYKFNALLVRYTKVPOVST 420
DB 384 CAKDDPHACYSTVPDKLHLVDEPNLKNQDQFELGEGYQFNALLVRYTKVPOVST 443
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEEDYLSVNLQCLVLRHEKTPVSDRVTKCCTES 480
DB 444 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEEDYLSVNLQCLVLRHEKTPVSDRVTKCCTES 503
QY 481 LVNRRPCFSALEVDVETVPKFEFNAETFTFHADICTLSEKERIQIKKQALVLRVHKPKAT 540
DB 504 LVNRRPCFSALEVDVETVPKFEFNAETFTFHADICTLSEKERIQIKKQALVLRVHKPKAT 563
QY 541 KEQLKAVMDDDFAFVEKCCADDKCTCFAGEGKLVAAASQAL 583
DB 564 EEQLKTVMENFVAFVDCCKAADDKCTCFAGEGKLVVSTQAL 606
RESULT 6
ABSHS
serum albumin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:90098888; PMID:2602160
A;Accession: S06936
A;Molecule type: mRNA
A;Residues: 1-607 <BRO>
A;Cross-references: EMBL:X17055; NID:q1386; PIDN:CAA34903.1; PID:q1387
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppe
teroid hormones (weak bonds with these hormones promote their transfer across the men
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: serum albumin #status predicted <MAT>
F;29-201/Domain: serum albumin repeat homology <SAL>
F;412-591/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-39
F;263/Binding site: bilirubin (Lys) #status predicted

Query Match

78.4%; Score 2432.5; DB 1; Length 607;

Best Local Similarity 75.0%; Pred. No. 1.8e-153;
Matches 437; Conservative 73; Mismatches 72; Indels 1; Gaps 1;

QY 1 DAHKEVAHFRKDLGEENFKALVLIAPAFYQYLOQCPEDHVKLVNEVTEFAKTCVADESA 60
Db 25 DTHKEIAHFRKDLGEENFGGLVLIAPAFYQYLOQCPEDHVKLVNEVTEFAKTCVADESA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 120
Db 85 GCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 143
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCOAAADKAACLLP 180
Db 144 DTLCAEFKADKEKFWGKYLEVARRHPYFYAPPELLYANKYNGVFOCCQAEDKGACLLP 203
QY 181 KLDELDEGKASSAKORLKASQKGERAFKAWAVARLSQRPFAEFAEVSCLVTLDTLK 240
Db 204 KIDAMREKVLASSARQLRCASIQKGERALKAMVARLSQKPKADFTDVTXIVTDLTK 263
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHTAIEVNDMPA 300
Db 264 VHKCECHGDLLECCADRADLAKYICDHQDALSCLKKECDKPVLEKSHCHTAIEVNDMPA 323
QY 301 DPLSLAADFVESKDVCKNYAEAKDVLGMFLFYEARHHPDYVSVLLRLAKTYETTLK 360
Db 324 NLPLTADAEADKEVKCNQYQKADVFLGSLFYESSRRHPYAVSVLLRLAKTYETTLK 383
QY 361 CAADPHCEYAKVDFEFLPVEPQNLKQNCFLPQLEGEYKFNQALLVRYTKVPQVST 420
Db 384 CAEDPHCEYAKVDFEFLPVEPQNLKQNCFLPQLEGEYKFNQALLVRYTKVPQVST 443
QY 421 PTLVEYSRLNGKVGSKCKHPEAKRMPCAEDYLSVNLCLVLEHTPTVSDRVTKCTES 480
Db 444 PTLVEYSRLNGKVGSKCKHPEAKRMPCAEDYLSVNLCLVLEHTPTVSDRVTKCTES 503
QY 481 LVNRFCFSALEVEDYTPVPEFNAETFTTHADICTLSEKREQIKKTALVELVKKHKKPAT 540
Db 504 LVNRFCFSALEVEDYTPVPEFNAETFTTHADICTLSEKREQIKKTALVELVKKHKKPAT 563
QY 541 KEOLKAVMDDFAEVKECKCKADKKECFEAEGKKLVAASQAAL 583
Db 564 DEQLKTMENFVAVDKCAADDEKGEVLEGPKLVAASQAAL 606

RESULT 7
ABRTS

serum albumin precursor - rat
N:Alternate names: preproalbumin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-May-1979 #sequence revision 31-May-1979 #text change 22-Jun-1999
C:Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R:Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 76, 243-246, 1981
A:Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A:Reference number: A93872; MUID:81223722; PMID:7017712
A:Accession: A93872
A:Molecule type: mRNA
A:Residues: 1-608 <SAR>
A:Cross-references: GB:V01222; GB:J00698; NID:g55627; PIDN:CAA24532.1; PID:g55628
R:Stauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
A:Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analysis
A:Reference number: A92211; MUID:77249657; PMID:893447
A:Note: cleavages during protein maturation
A:Accession: A92211
A:Molecule type: protein
A:Residues: 1-38 <STR>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A:Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A:Reference number: A91946; MUID:78109429; PMID:564345
A:Accession: A91946
A:Molecule type: protein

A:Residues: 25-222 <ISL>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 79, 1183-1196, 1976
A:Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino
A:Reference number: A91940; MUID:76260153; PMID:956149
A:Accession: A91940
A:Molecule type: protein
A:Residues: 223-288:572-608 <IS2>
A:Note: 262-Leu was also found
R:Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A:Title: Copper(II)-binding ability of human alpha-fetoprotein.
A:Reference number: A90758; MUID:79001617; PMID:80265
A:Contents: annotation; Copper binding
R:Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid prot
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: C45800
A:Status: preliminary
A:Molecule type: protein
A:Residues: 166-173 <CAR>
R:Heard, J.
Mol. Cell. Biol. 7, 2425-2434, 1987
A:Title: Determinants of rat albumin promoter tissue specificity analyzed by an impro
A:Reference number: I57621; MUID:87286876; PMID:3475566
A:Accession: I57621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M16825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:19-24/Domain: signal sequence #status experimental <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:225-608/Product: serum albumin #status experimental <SA1>
F:221-394/Domain: serum albumin repeat homology <SA1>
F:413-592/Domain: serum albumin repeat homology <SA2>
F:27/Binding site: copper (His) #status experimental
F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-39

Query Match 78.2%; Score 2426; DB 1; Length 608;
Best Local Similarity 73.4%; Pred. No. 4.7e-153;
Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;

QY 1 DAHKEVAHFRKDLGEENFKALVLIAPAFYQYLOQCPEDHVKLVNEVTEFAKTCVADESA 60
Db 25 EAHKEIAHFRKDLGEENFGGLVLIAPAFYQYLOQCPEDHVKLVNEVTEFAKTCVADENA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 144
QY 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCOAAADKAACLLP 180
Db 145 EAMCTSFQENPTSFGLHYLHEVARRHPYFYAPPELLYAEKYNEVLTQCTESDKAACLTP 204
QY 181 KLDELDEGKASSAKORLKASQKGERAFKAWAVARLSQRPFAEFAEVSCLVTLDTLK 240
Db 205 KLDVCKERKALVAARVQRKSSMQRGGERAFKAWAVARMSQRPFAEFAEITKATDVTK 264
QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHTAIEVNDMPA 300
Db 265 INKECHGDLLECCADRADLAKYICENQDSISSKLEKCECKPLEKSHCHTAIEVNDMPA 324
QY 301 DPLSLAADFVESKDVCKNYAEAKDVLGMFLFYEARHHPDYVSVLLRLAKTYETTLK 360
Db 325 DPLSLAADFVESKDVCKNYAEAKDVLGMFLFYEARHHPDYVSVLLRLAKTYETTLK 384
QY 361 CAADPHCEYAKVDFEFLPVEPQNLKQNCFLPQLEGEYKFNQALLVRYTKVPQVST 420
Db 385 CAEGDPPACVGTVAEFQPLVEEPKLVKTNCELYEKLGEYGFQNAVLRVYTKQAPQVST 444

Db 330 LPSLVKEKVEDKVSPEAGHDAPMAEFVVEYSRRHPFESLIQIMRIAKGVESLLEKCC 389

QY 362 AAADPHECYAKVDFEKLVEEONLIKONCELFQIGYKFNALLVRYTKYPOVSTP 421

Db 390 KTDNPAECYANAEOQNHQIKETQDVVNTCDLHHDGEADFLSKILRYTKMPOVPTD 449

QY 422 TLVEVSRNLGVSKCKKHPKAPCAEDYLSVNLQCLVHLHEKTPVSDRVTKCTESL 481

Db 450 LLLGTGKMTTIGTKCCQGLGDRMACSEGLSVIHDTCRKQETTPINDNVSCCSQLY 509

QY 482 VNRRCFSALEVDETYVPKFNAAETFFHADICILSEKERQIKKQTALVELVKHKPKATK 541

Db 510 ANRRCFTAMGVDTKYVPPFNPDMFSEDEKLCSAPAEEREVGQMKLLINLIKRPQMT 569

QY 542 EQLKAVMDDFAAVFKCKKADDKETCFABEGGKLVAAASQAALGL 585

Db 570 EQIKTIAGFTAMWDKCKQSDINTCFGEAGNLIVQSRATLGI 613

RESULT 12

JC4258

alpha-fetoprotein precursor - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C:Date: 27-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999

C:Accession: JC4258

R:Nishio, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczky, A.

Gene 162, 213-220, 1995

A:Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to

A:Reference number: JC4258; MUID:96032345; PMID:7557431

A:Accession: JC4258

A:Molecule type: DNA

A:Residues: 1-609 <NTS>

A:Cross-references: GB:U21916; NID:g841311; PIDN:AAA91641.1; PID:g841312

A:Comment: This protein is a plasma protein produced in the fetal and neonatal liver and

o similar properties and structure.

C:Genetics:

A:Gene: afp

A:Map position: 3p

A:Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 553/

A:Superfamily: serum albumin; serum albumin repeat homology

C:Keywords: glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-609/Product: alpha-fetoprotein #status predicted <MAT>

F:29-202/Domain: serum albumin repeat homology <SA1>

F:221-394/Domain: serum albumin repeat homology <SA2>

F:413-592/Domain: serum albumin repeat homology <SA3>

F:42,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.4%; Score 1253.5; DB 2; Length 609;

Best Local Similarity 40.1%; Pred. NO. 1.9e-75;

Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

QY 3 HKSE-----VAHRFDLGEENFKALVLAFAQYLOQCFEDHVKLVNEVTEFAKTCVADE 57

Db 22 HRNEYGIASILDSYQCTAEINTDLATIFFAQVQETATYKEVSKVMKDALTAIERPTGDE 81

QY 58 SAENDCKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNP-NLPLV 116

Db 82 QSAGCLENQLPAFLBELCREKLEIKYGH-SDCCSQSSEGRNCFLAHKKPTPASPFPFO 140

QY 117 RPEVDMCTAFHDNEETFLKKLYEITARRHPFYFAPELLFFAKRYKAAFTCCQAADKAA 176

Db 141 VPEPVTSCAYEEDRETFMNKFYETIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE 200

QY 177 CLLPKLDELDRGKASSAKQRLKASLOKFGGERAFKANAVARLSORFPKAEFAEVSCLVT 236

Db 201 CFQTKAATVTKELRESSLLNQHACAVMKNFGRTRTEQAITVTLSQKFTKVNTEIQKLVL 260

QY 237 DLTQVHTECHGDLLECADRADLAKYICENODSISKKLKECCERPLEKSKHICAEVND 296

Db 261 DVAHVHECCRGDVLDCLODGEKIMSYICSQODTILSNKITECCKUTTLDERGQCIHAEND 320

QY 297 EMPADPLSLAADFVESKDVCKNYABAKDVLGMLFLEYARRHPDYSVVLRLAKTYETT 356

Db 321 EKPEGLSPNLNRLGDRDNFQFSGEKNIFLASFVHEYSRRHPQLAVSVILRVAKGYOEL 380

QY 357 LEKCCAAADPHECYAKVDFEKLVEEONLIKONCELFQIGYKFNALLVRYTKKVP 416

Db 381 LEKCFQETNPELECODKGBEELQKYIQESQALAKRSGGLFQKLGLEYLQNALVATVKKAP 440

QY 417 QVSTPTLVESVRNLGVSKCKKHPKAPCAEDYLSVNLQCLVHLHEKTPVSDRVTKC 476

Db 441 QLTSSSELMAITRKMAATAATCCQLSEDKLLACGEAADIIGHLCIRHETTPVNGVGC 500

QY 477 CTESLVNRRPFCFALEVDETYVPKFNAAETFFHADICILSEKERQIKKQTALVELVKHK 536

Db 501 CTSSVANRRPFCSSLVVDETYVPPAFSDDKETIFHDKLQCAQGVALQTKQEFNLINLVKQ 560

QY 537 PKATKEQLKAVMDDFAAVFKCKKADDKETCFABEGGKLVAAASQAALGL 585

Db 561 FOITEEQLEAVIADFSGLLKCCQCEQEVFAEEGQKLISKTRALGV 609

RESULT 13

PFHU

alpha-fetoprotein precursor [validated] - human

N:Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 08-Dec-2000

C:Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042;

R:Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczky, A.

Biochemistry 26, 1332-1343, 1987

A:Title: Structure, polymorphism, and novel repeated DNA elements revealed by a compl

A:Reference number: A26624; MUID:87185438; PMID:2436661

A:Accession: A26624

A:Molecule type: DNA

A:Residues: 1-609 <GTB>

A:Cross-references: GB:M16110; NID:g773678; PIDN:AA58754.1; PID:g178236

R:McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Kruml

Hum. Mol. Genet. 2, 379-384, 1993

A:Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein

A:Reference number: S37655; MUID:93278385; PMID:7684942

A:Accession: S37655

A:Molecule type: DNA

A:Residues: 1-28 <MCV>

A:Cross-references: EMBL:Z19532; NID:g28527; PIDN:CAA79592.1; PID:g28528

A:Note: the authors translated the codon TAT for residue 26 as Thr

R:Morinaga, T.; Sakai, M.; Wegmann, T.G.; Tamaoki, T.

Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983

A:Title: Primary structures of human alpha-fetoprotein and its mRNA.

A:Reference number: A93961; MUID:83273664; PMID:6192439

A:Accession: A93961

A:Molecule type: mRNA

A:Residues: 1-609 <MOR>

A:Cross-references: GB:J00077; NID:g311348; PIDN:CAA24758.1; PID:g31351

R:Beattie, W.G.; Dugaiczky, A.

Gene 20, 415-422, 1982

A:Title: Structure and evolution of human alpha-fetoprotein deduced from partial sequ

A:Reference number: A91497; MUID:83158778; PMID:6187626

A:Accession: A91497

A:Molecule type: mRNA

A:Residues: 429-556 <BEA>

A:Cross-references: GB:J00076

R:Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.; Terr

Biochemistry 30, 5061-5066, 1991

A:Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.

A:Reference number: A23699; MUID:91242409; PMID:1709810

A:Accession: A23699

A:Molecule type: protein

A:Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>

R:Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.

J. Nucl. Med. Allied Sci. 34, 213-216, 1990

A:Title: Characterization of in vitro expressed human alpha-fetoprotein as highly rep

A:Reference number: A61480; MUID:91225826; PMID:1709209

A:Accession: A61480

A:Molecule type: protein

Db 141 VPEPVTSEAYEEDRETFMNFYIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE 200
 Qy 177 CLLPLDLRLDEBKGASSAKQRLKASLOKFGGERAFKANAVARLSORFEPKAEFAEYSKLVT 236
 Db 201 CFQTKAAVTRELRESSLNQHACAVMKNFGTRTQATVTKLSOKFTKVNFEIQLVL 260
 Qy 237 DUTKVHTECCGDLLEADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVEND 296
 Db 261 DVAVHVEHCCRGDVLCDLQDGBEKINSYCSQDITLSNKITECKLTTLERGQIIHAEND 320
 Qy 297 ENPADLPSLAADFVESKCVKNYAKADVFLGMFLYEVARRHPDYSVLLLLAKTYETT 356
 Db 321 EKPEGLSPNLNRLGDRDFNFSSEKNIIFLASFYHESRRHPQLAVSVILRVAKGYOEL 380
 Qy 357 LEKCCAAADPHCYAKVDFEFLPELVPEPNLIKONCELFQELGVEYKFNALLVRYTKVP 416
 Db 381 LEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGYYLQNAFLVATYTKRP 440
 Qy 417 QVSTPLVEVSRNLKGVSKCKKHPKAEKMPCAEDYLSVNLQCLVHLKEKTPVSDRVTKC 476
 Db 441 QLTSSLMATRKMAATAATCCQLSEDKLLACGEGAADIIGHLCIRHEMTFVNPVGVQC 500
 Qy 477 CTESLVNRRPFSALEVDETYVPKEFNAETFTFHADICTLSKERQIKQTALVELVKHK 536
 Db 501 CTSSVANRRPCFSSLVVDETYVPPAFSDDKFTFHKDLQCAQGVALQTMKQEFNLNVRKQ 560
 Qy 537 PKATKEQLKAVMDFAAEVEKCKADDKETCFAEKGLKLVAAQAAGL 585
 Db 561 POITEEQLETVIADPSGLLEKCKCGQEQEVCFAEQGLSKLTKRTALGV 609

RESULT 15
 ABXL72
 74K albumin precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: B41682; S02693; A05288
 R:Moskatis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
 Mol. Endocrinol. 3, 464-473, 1989
 A:Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid during development.
 A:Reference number: A41682; MUID:89313788; PMID:2747653
 A:Accession: B41682
 A:Molecule type: mRNA
 A:Residues: 3-607 <MOS>
 A:Cross-references: GB:M21442; NID:g213930; PIDN:AAA49637.1; PID:g213931
 R:Schorpp, M.; Doebebling, U.; Wagner, U.; Ryffel, G.U.
 J. Mol. Biol. 199, 83-93, 1988
 A:Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Deletion of the 5'-flanking region of the 5'-proximal exon results in a non-functional gene.
 A:Reference number: S02692; MUID:88172470; PMID:2451026
 A:Accession: S02693
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-48 <SCH>
 A:Cross-references: EMBL:Z26826
 R:Wolfe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J.
 Eur. J. Biochem. 146, 489-496, 1985
 A:Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilization of the 5'-proximal exon results in a non-functional gene.
 A:Reference number: A05288; MUID:85126974; PMID:3971963
 A:Accession: A05288
 A:Molecule type: mRNA
 A:Residues: 459-502, 'L' 504-557 <WOL>
 A:Cross-references: GB:M28276
 A:Note: The authors translated the codon TAT for residue 63 as Thr
 C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, molybdenum, and zinc ions. It is secreted into the blood stream where it is converted to albumin by the removal of the signal sequence.
 C:Genetics:
 A:Introns: 27/1
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>

F:25-607/Product: 74K serum albumin #status predicted <MAT>
 F:320-201/Domain: serum albumin repeat homology <SA1>
 F:320-393/Domain: serum albumin repeat homology <SA2>
 F:412-591/Domain: serum albumin repeat homology <SA3>
 F:30/Binding site: copper (His) #status predicted
 F:80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-384
 F:256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.8%; Score 1205; DB 1; Length 607;
 Best Local Similarity 39.3%; Pred No. 3e-72;
 Matches 227; Conservative 108; Mismatches 239; Indels 4; Gaps 2;

Qy 3 HKSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPFFDHVKLVNEVTEFAKTCAVDESAENC 62
 Db 30 HHKHIADVYALTERTFKGLTIAIVSONLQKCSLELSKLVNEINDFAKSINDKTPC-C 88
 Qy 63 DKSILHTLFGDKLCTVATLRETYGEMADCCAKOBERNECFLOHKDNPRLVPRPEVDV 122
 Db 89 EKPVGTLFFDKLCAADPAVGVNVEYSEKCAQKQDPERAOQCFKAHRDHEHT---SIKPEPEE 145
 Qy 123 MCTAFHDNEETFLKKVLYEIAARRHPVYFAPELLFTFAKRYKAAFTCCCAADKAACLLPKL 182
 Db 146 TCKLLKEHPDDLLSAFIIHEARNHPDLYPPAVIALTKQTHKLAHCEDEEDKEKCFSEKM 205
 Qy 183 DELRDEGRASSAKQRLKASLOKFGGERAFKANAVARLSORFEPKAEFAEYSKLVTDLTKVH 242
 Db 206 KOLMKQSHSIEDKQHFHCWILONFPEKVLKALNARVSHRYPKAEKLAHNTEEVTHFI 265
 Qy 243 TECCHGDLLEADRADLAKYICENODSISKLKECCERPLLEKSHCIAEVENDEMPADL 302
 Db 266 KDCCHDDMFECMTERLELTHCTQHKDELSSKLEKCCNIPLEERTYCIIVLENDVPAEL 325
 Qy 303 PSLAADVESKDVCKNYAEAKDVLGMFLYEVARRHPDYSVLLLLRLAKTYETTLEKCCA 362
 Db 326 SPTITEFTEDPHVCBKAYAEENNEVFLGRYLHAVSRKHQELSEDFLOSAKEYESLNNKCK 385
 Qy 363 AADPHECYAKVDFEFLPELVPEPNLIKONCELFQELGVEYKFNALLVRYTKVPQVSTPT 422
 Db 386 TDNPPECYKOGADRFENAEKRFAYLKQNCIDLHEGELYFENELLIRYTKMPQVSDET 445
 Qy 423 LVEVSRNLKGVSKCKKHPKAEKMPCAEDYLSVNLQCLVHLKEKTPVSDRVTKCCTESLV 482
 Db 446 LIGIAHOMADIGEHCACVAPNQMPCAEGLTILIGKMCERQKKTFINNHVACCTDSYS 505
 Qy 483 NRPFCFSALEVDETYVPKEFNAETFTFHADICTLSKERQIKQTALVELVKHKPRATKE 542
 Db 506 GMRSCFTALGPDEDYVPPVPTDTHFDKICTADKEKQHKQKFLVLIKVPKLEKN 565
 Qy 543 QLKAVMDFAAEVEKCKADDKETCFAEKGLKLVAAASQ 580
 Db 566 HIDECSAEFLKMWQKCCCTADEHQPCFDTKEKPVLEHCQ 603

Search completed: April 24, 2003, 07:23:12
 Job time : 24 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:18 ; Search time 14 Seconds
(without alignments)
1733.118 Million cell updates/sec

Title: us-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHKSEVAHRFKDLGEENFK.....TCFAEGCKLVAASQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3103	100.0	609	1	ALBU_HUMAN
2	2942	94.8	600	1	ALBU_MACMU
3	2620	84.4	608	1	ALBU_FELCA
4	2562	82.6	608	1	ALBU_CANFA
5	2475.5	79.8	607	1	ALBU_HORSE
6	2450.5	79.0	607	1	ALBU_BOVIN
7	2446	78.8	608	1	ALBU_RABIT
8	2432.5	78.4	607	1	ALBU_SHEEP
9	2426	78.2	608	1	ALBU_RAT
10	2411.5	77.7	605	1	ALBU_PIG
11	2387	76.9	609	1	ALBU_MERUN
12	2378	76.6	608	1	ALBU_MOUSE
13	1557.5	50.2	615	1	ALBU_CHICK
14	1233.5	40.4	609	1	FETA_PANTR
15	1249.5	40.3	609	1	FETA_HUMAN
16	1242.5	40.0	609	1	FETA_GORGO
17	1205	38.8	607	1	ALBU2_XENLA
18	1200	38.7	609	1	FETA_HORSE
19	1164.5	37.5	605	1	ALBU1_XENLA
20	1084	34.9	605	1	FETA_MOUSE
21	1067	34.4	611	1	FETA_RAT
22	1055	34.0	599	1	AFAM_HUMAN
23	944	30.4	611	1	AFAM_MOUSE
24	928	29.9	608	1	AFAM_RAT
25	747.5	24.1	608	1	ALBU1_SALSA
26	742.5	23.9	608	1	ALBU2_SALSA
27	699	22.5	382	1	ALBU_RANCA
28	440.5	14.2	1423	1	ALBU1_PETMA
29	386	12.4	474	1	VTDB_HUMAN
30	381	12.3	476	1	VTDB_RAT
31	378	12.2	476	1	VTDB_RABIT
32	372	12.0	472	1	VTDB_MOUSE
33	133.5	4.3	1391	1	MSTL2_DROHY

RESULT 1

ID	ALBU_HUMAN	STANDARD	PRT	609 AA
AC	P02768; Q13140; Q9UJ20; Q9UHS3; Q9P117; Q9P157; Q9S574;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Serum albumin precursor.			
GN	ALB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=86196112; PubMed=3009475;			
RX	Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,			
RA	Beattie W.G., Dugaiczak A.;			
RT	"Molecular structure of the human albumin gene is revealed by			
RT	nucleotide sequence within q11-22 of chromosome 4.";			
RL	J. Biol. Chem. 261:6747-6757(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82081882; PubMed=6171778;			
RA	Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,			
RA	Najarian R.C., Seeburg P.H., Wion K.L.;			
RT	"The sequence of human serum albumin cDNA and its expression in E.			
RT	coli.";			
RL	Nucleic Acids Res. 9:6103-6114(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82105994; PubMed=6275391;			
RA	Dugaiczak A., Law S.W., Dennison O.E.;			
RT	"Nucleotide sequence and the encoded amino acids of human serum			
RT	albumin mRNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Liver;			
PC	Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;			
RA	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Fetal liver;			
RA	Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,			
RA	He F.;			
RT	"Functional prediction of the coding sequences of 79 new genes deduced			
RT	by analysis of cDNA clones from human fetal liver.";			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 25-609.			
RX	MEDLINE=76187907; PubMed=1225573;			
RA	Meloun B., Moravsek L., Kostka V.;			
RT	"Complete amino acid sequence of human serum albumin.";			
RL	FEBS Lett. 58:134-137(1975).			
RN	[7]			

ALIGNMENTS

RP SEQUENCE OF 25-609.
 RA Brown J.R., Shockley P., Behrens P.Q.;
 RL (in) Bing D.H. (eds.);
 RL The chemistry and physiology of the human plasma proteins, pp.23-40,
 RL Pergamon Press, New York (1979).
 RN [8]
 RP SEQUENCE OF 1-455 FROM N.A.
 RC TISSUE=Liver;
 RA Menaya J., Parrilla R., Ayuso M.S.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A. (PRO2619/PRO2044/PRO1708/PRO2675).
 RC TISSUE=Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
 RA Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
 RT "Functional prediction of the coding sequences of 121 new genes
 RT deduced by analysis of cDNA clones from human fetal liver";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE OF 1-26 FROM N.A.
 RC TISSUE=Liver;
 RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
 RL "The human albumin gene. Characterization of the 5' and 3' flanking
 RT regions and the polymorphic gene transcripts.";
 RL J. Biol. Chem. 261:3244-3251(1986).
 RN [11]
 RP SEQUENCE OF 222-229.
 RC TISSUE=Liver;
 RA Walker J.E.;
 RL "Lysine residue 199 of human serum albumin is modified by
 RT acetylcholinesterase";
 RL FEBS Lett. 66:173-175(1976).
 RN [12]
 RP SEQUENCE OF 25-44 AND 480-499.
 RC TISSUE=Heart;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [13]
 RP SEQUENCE OF 409-609 FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP DISULFIDE BONDS.
 RA Saber M.A., Stockbauer P., Moravsek L., Meloun B.;
 RL "Disulfide bonds in human serum albumin";
 RL Collect. Czech. Chem. Commun. 42:564-579(1977).
 RN [15]
 RP BILIRUBIN-BINDING SITE.
 RA Jacobsen C.;
 RL "Lysine residue 240 of human serum albumin is involved in high-
 RT affinity binding of bilirubin";
 RL Biochem. J. 171:453-459(1978).
 RN [16]
 RP VARIANT CANTERBURY.
 RA MEDLINE=87157744; PubMed=3828358;
 RA Brennan S.O., Herbert P.;
 RT "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second
 RT domain of serum albumin";
 RL Biochim. Biophys. Acta 912:191-197(1987).
 RN [17]
 RP VARIANTS NAG-2 AND NAG-3.
 RA MEDLINE=88068523; PubMed=3479777;
 RA Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
 RA Satoh C., Neel J.V.;
 RT "Amino acid substitutions in inherited albumin variants from
 RT Amerindian and Japanese populations";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
 RN [18]

RP VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
 RX MEDLINE=89345611; PubMed=2762316;
 RA Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M.,
 RA Neel J.V., Sakurabayashi I., Putnam F.W.;
 RT "Point substitutions in Japanese albumins";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
 RN [19]
 RP VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
 RX MEDLINE=90115905; PubMed=2404284;
 RA Arai K., Madison J., Shimizu A., Putnam F.W.;
 RT "Point substitutions in albumin genetic variants from Asia";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
 RN [20]
 RP VARIANT REDHILL.
 RX MEDLINE=90115852; PubMed=2104980;
 RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
 RT "Human Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
 RT albumin serum albumin whose precursor has an aberrant signal peptidase
 RT cleavage site";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
 RN [21]
 RP VARIANTS TORINO; VARESE AND VIBO VALENTIA.
 RX MEDLINE=91062352; PubMed=2247440;
 RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
 RA Watkins S., Putnam F.W.;
 RT "Mutations in genetic variants of human serum albumin found in
 RT Italy";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
 RN [22]
 RP VARIANT VENEZIA.
 RX MEDLINE=91296740; PubMed=2068071;
 RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
 RA Minchiotti L., Putnam F.W.;
 RT "A donor splice mutation and a single-base deletion produce two
 RT carboxyl-terminal variants of human serum albumin";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
 RN [23]
 RP VARIANTS IOWA CITY AND KOMAGOME.
 RX MEDLINE=92052189; PubMed=1946412;
 RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
 RA Matsuda Y.-I., Amaki I., Putnam F.W.;
 RT "Genetic variants of serum albumin in Americans and Japanese";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
 RN [24]
 RP VARIANT CASEBROOK.
 RX MEDLINE=91316157; PubMed=1859851;
 RA Peach R.J., Brennan S.O.;
 RT "Structural characterization of a glycoprotein variant of human serum
 RT albumin: albumin Casebrook (494 Asp-->Asn)";
 RL Biochim. Biophys. Acta 1097:49-54(1991).
 RN [25]
 RP VARIANTS SONDRIO AND PARIS-2.
 RX MEDLINE=92190239; PubMed=1347703;
 RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
 RA Rochu D., Porta F.;
 RT "Two albumins with identical electrophoretic mobility are produced
 RT by differently charged amino acid substitutions";
 RL Biochim. Biophys. Acta 1119:232-238(1992).
 RN [26]
 RP VARIANTS MALMO.
 RX MEDLINE=92390419; PubMed=1518850;
 RA Carlson J., Sakamoto Y., Laurell C.-B., Madison J., Watkins S.,
 RA Putnam F.W.;
 RT "Alloalbuminemia in Sweden: structural study and phenotypic
 RT distribution of nine albumin variants";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8225-8229(1992).
 RN [27]
 RP VARIANT HERBORN.
 RX MEDLINE=93292504; PubMed=8513793;
 RA Minchiotti L., Galliano M., Zapponi M.C., Tenni R.;
 RT "The structural characterization and bilirubin-binding properties of
 RT albumin Herborn, a [Lys240-->Glu] albumin mutant";
 RL Eur. J. Biochem. 214:437-444(1993).

```

Query Match      100.0%; Score 3103; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.7e-195;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 84
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLVRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLVRPEV 144
Qy 121 DVMCTAFHDNEETFLKYLVIATIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 145 DVMCTAFHDNEETFLKYLVIATIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 204
Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 205 KLDELDRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 264
Qy 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCCKPILLESKSHCIAEVENDEMPA 300
Db 265 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCCKPILLESKSHCIAEVENDEMPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEXARRHPDYSVVLLRLAKTYETTLK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEXARRHPDYSVVLLRLAKTYETTLK 384
Qy 361 CAADPHECYAKVDFEKPVLVEEPQNLIKONCELFGEQYKFNALLVRYTKVPQVST 420
Db 385 CAADPHECYAKVDFEKPVLVEEPQNLIKONCELFGEQYKFNALLVRYTKVPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRVTKCCTES 504
Qy 481 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQALVELVHKPKAT 540
Db 505 LVNRRPFCFSALEVDVETVPKFEFNAETTFHADICTLSEKERQIKKQALVELVHKPKAT 564
Qy 541 KEQLKAVMDPFAAFVEKCCCKADKTCFAEKGKLVLAASQAALGL 585
Db 565 KEQLKAVMDPFAAFVEKCCCKADKTCFAEKGKLVLAASQAALGL 609

RESULT 2
ID ALBU_MACMU STANDARD; PRT; 600 AA.
AC Q28522;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211971; PubMed=8460152;
RA Watkins S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,
RA Dwalet J., Putnam F.W.;
RT "cDNA and protein sequence of polymorphic macaque albumins that differ
RT in bilirubin binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.

```

```

CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M90463; AAA36906.1; -
CC HSP; P02768; 1E7B.
CC InterPro: IPR000264; Serum_albumin.
CC Pfam: PF00273; transport_prot; 3.
CC ProDom: PD002486; Serum_albumin; 1.
CC SMART: SM00103; ALBUMIN; 3.
CC PROSITE: PS00212; ALBUMIN; 3.
CC Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
CC Copper.
CC -----
CC 1 1
CC SIGNAL <1 10 BY SIMILARITY.
CC PROPEP 11 16 BY SIMILARITY.
CC CHAIN 17 600 SERUM ALBUMIN.
CC DOMAIN 17 197 ALBUMIN 1.
CC DOMAIN 204 389 ALBUMIN 2.
CC DOMAIN 396 587 ALBUMIN 3.
CC METAL 19 19 COPPER (BY SIMILARITY).
CC BINDING 256 256 BILIRUBIN (POTENTIAL).
CC DISULFID 61 78 BY SIMILARITY.
CC DISULFID 91 107 BY SIMILARITY.
CC DISULFID 106 117 BY SIMILARITY.
CC DISULFID 140 185 BY SIMILARITY.
CC DISULFID 184 193 BY SIMILARITY.
CC DISULFID 216 262 BY SIMILARITY.
CC DISULFID 261 269 BY SIMILARITY.
CC DISULFID 281 295 BY SIMILARITY.
CC DISULFID 294 305 BY SIMILARITY.
CC DISULFID 332 377 BY SIMILARITY.
CC DISULFID 376 385 BY SIMILARITY.
CC DISULFID 408 454 BY SIMILARITY.
CC DISULFID 453 464 BY SIMILARITY.
CC DISULFID 477 493 BY SIMILARITY.
CC DISULFID 492 503 BY SIMILARITY.
CC DISULFID 530 575 BY SIMILARITY.
CC DISULFID 574 583 BY SIMILARITY.
CC SEQUENCE 600 AA; 67880 MW; E45C871A670E740B CRC64;
Query Match      94.8%; Score 2942; DB 1; Length 600;
Best Local Similarity 93.5%; Pred. No. 8.3e-185;
Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 17 DTHKSEVAHREFKDLGEENFKALVLIATFAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAAE 76
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLVRPEV 120
Db 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOPEPERNECFLOHKDDNPMLPLVRPEV 136
Qy 121 DVMCTAFHDNEETFLKYLVIATIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
Db 137 DVMCTAFHDNEETFLKYLVIATIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADKAACLLP 196
Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 240
Db 197 KLDELDRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSQRFPAEFAEVSCLVTDLT 256
Qy 241 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCCKPILLESKSHCIAEVENDEMPA 300
Db 257 VHTCCCHGDLLECADRADLAKYICENODSISSKLKECCCKPILLESKSHCIAEVENDEMPA 316

```

QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 360
Db 317 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKAYEATLEK 376
QY 361 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPQVST 420
Db 377 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPQVST 436
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRYTKCCTES 480
Db 437 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSEKVTKCCTES 496
QY 481 LVNRRPFCFSALEYDEYVVPKFEAFNAETFTPHADICTLSEKERQIKKQTALVELVKKHPRKAT 540
Db 497 LVNRRPFCFSALEYDEYVVPKFEAFNAETFTPHADICTLSEKERQIKKQTALVELVKKHPRKAT 556
QY 541 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 583
Db 557 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 599

RESULT 3
ALBU_FELCA STANDARD; PRT: 608 AA.
AC P49064;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Fel d 2).
GN ALB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96194824; PubMed=8647469;
RA Hilger C., Grigioni F., Kohnen M., Hentges F.;
RT "Sequence of the gene encoding cat (Felis domesticus) serum albumin.";
RL Gene 169,295-296(1996).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: X84842; CAA59279.1;
DR HSP: P02768; 1E7B.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper; Allergen.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.

FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
SQ SEQUENCE 608 AA; 68659 MW; 07E629CAC3F60B5F CRC64;

Query Match 84.4%; Score 2620; DB 1; Length 608;
Best Local Similarity 82.0%; Pred. No. 8 4e-164;
Matches 478; Conservative 52; Mismatches 53; Indels 0; Gaps 0;
QY 1 DAHKEVAHFRKDLGBENFKALVLIAPAOYLOQCPEDHVKLVNVEYTEFAKTCVADESAAE 60
Db 25 EAHQSEIAHFRNDLGBEHPRLVLFVAFVSOYLOQCPEDHVKLVNVEYTEFAKTCVADESAA 84
QY 61 NCDKSLHTLFGDKLCIVATLRETYGEMADCCAKQEBERNECFLOHKDDNPNLRLVPRPEV 120
Db 85 NCKSLHLLGDKLCTVASLRDKYGMADCCCKEKEPERNECFLOHKDDNPNLRLVPRPEV 144
QY 121 DVNCTAFHNDNEETFLKLYEIAIRRHYPFYAPPELLFYAPPELLFYAPPELLFYAPPELLFY 180
Db 145 DAMCTAFHNEQRFGLKLYEIAIRRHYPFYAPPELLFYAPPELLFYAPPELLFYAPPELLFY 204
QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFKAWAVARLSORPKAEFAEVSCLVTDLT 240
Db 205 KVDALREKVLASSAKERLKCASLQKFGERAFKAWAVARLSORPKAEFAEVSCLVTDLT 264
QY 241 VHECCGHDLECCADDRADLAKYICENQDSISSKKECCCKPILLESKSHCTAEVENDMPA 300
Db 265 IHKECCGHDLECCADDRADLAKYICENQDSISSKKECCCKPILLESKSHCTAEVENDMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 360
Db 325 DLPLAVDFVEDKEVCKNYEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLK 384
QY 361 CAADPHCEYAKVDFEKPPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPQVST 420
Db 385 CATDDPPACVYHVFDEKPLVEBPQNLKONCELFQOLGEYKFNALLVRYTKVPQVST 444
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRYTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRYTKCCTES 504
QY 481 LVNRRPFCFSALEYDEYVVPKFEAFNAETFTPHADICTLSEKERQIKKQTALVELVKKHPRKAT 540
Db 505 LVNRRPFCFSALEYDEYVVPKFEAFNAETFTPHADICTLSEKERQIKKQTALVELVKKHPRKAT 564
QY 541 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 583
Db 565 KEOLKAVMDFAAFVEKCKKADDEKTCFADEGKGLVNAASQAAL 607

RESULT 4
ALBU_CANFA STANDARD; PRT: 608 AA.
ID ALBU_CANFA
AC P49822; O77705; Q9TS24;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Can f 3).

GN ALB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RA Hilger C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20148667; PubMed=1069848;
RA Pandjaitan B., Swoboda I., Brandesky-Pichler F., Rumpold H.,
Valenta R., Spitzauer S.;
RT "Escherichia coli expression and purification of recombinant dog
albumin, a cross-reactive animal allergen.";
RN J. Allergy Clin. Immunol. 105:279-285(2000).
RL [3]
RP SEQUENCE OF 25-48.
RX MEDLINE=75011422; PubMed=4414013;
RA Dixon J.W., Sarkar B.;
RT "Isolation, amino acid sequence and copper(II)-binding properties of
peptide (1-24) of dog serum albumin.";
RN J. Biol. Chem. 249:5872-5877(1974).
RL [4]
RP SEQUENCE OF 25-38.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
RN [5]
RP SEQUENCE OF 215-478 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94201492; PubMed=7512102;
RA Spitzauer S., Schweizer C., Sperr W.R., Pandjaitan B., Valent P.,
Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
RT "Molecular characterization of dog albumin as a cross-reactive
allergen.";
RL J. Allergy Clin. Immunol. 93:614-627(1994).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ133489; CAB64867.1; -;
DR EMBL; Y17737; CAAT76841.1; -;
DR EMBL; S72946; AAB30434.1; -;
DR PIR; S29749; S29749.
DR HSP; P02768; 1E7B.
DR HSC-2DPAGE; P49822; DOG.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;

Copper; Allergen.
KW SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 608
FT DOMAIN 25 205
FT DOMAIN 212 397
FT DOMAIN 404 595
FT METAL 27 27
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 148 193
FT DISULFID 192 201
FT DISULFID 224 270
FT DISULFID 269 277
FT DISULFID 289 303
FT DISULFID 302 313
FT DISULFID 340 385
FT DISULFID 384 393
FT DISULFID 416 462
FT DISULFID 461 472
FT DISULFID 485 501
FT DISULFID 500 511
FT DISULFID 538 583
FT DISULFID 582 591
FT CONFLICT 1 26
FT CONFLICT 146 146
FT CONFLICT 206 206
FT CONFLICT 349 349
FT CONFLICT 359 359
FT CONFLICT 448 448
FT CONFLICT 474 474
SQ SEQUENCE 608 AA; 68606 MW; 3C1C8FF7DD8FC06 CRC64;
Query Match 82.6%; Score 2562; DB 1; Length 608;
Best Local Similarity 79.8%; Pred. No. 5,1e-160;
Matches 465; Conservative 57; Mismatches 61; Indels 0; Gaps 0;
QY 1 DAHSEVAVRFDLGEENFKALVLIATAFYLOQCPEDHVKLVNTEFAKTCAVDESAE 60
DB 25 EAYKSEIAHYNDLGEHFRGLVAVFSQYLOQCPEDHVKLVNTEFAKTCAVDESAG 84
QY 61 NCDKSLHTLFGDKLCTVATIRETYGEMADCCAKOEPEERNECFQHKDDNPNLRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVASLRDKYGMADCCKEQEDRNECFQHKDDNPNLVRPEV 144
QY 121 DVNCTAFHDNEETFLKKYLYETARRHPYFAPPELLFFAKRYKAAFTCCOAAKACLLP 180
DB 145 DALCAAFQDNEQLFLGKLYLYETARRHPYFAPPELLFYAQQYKGVFAECCQAADKACLP 204
QY 181 KLDELDEGKASSAKORLKCASLOKGEFRAKAWARLSQREPKAFEAHSVSLVTDLT 240
DB 205 KIEALREKVLSSAKERFKCASLOKGEFRAKAWARLSQREPKAFEAHSVSLVTDLT 264
QY 241 VITECHGDLLECCADRADLAKYICENQDSISSKLECEKPLEKSHCIAEVENDEMPA 300
DB 265 VHKCECHGDLLECCADRADLAKYICENQDSISITKLECCDKPVLEKSQCLAEVERDELPG 324
QY 301 DLPSLAADVESKDVCKNYAEAKDVLGMFLYETARRHPDYSVLLLRLLAKTYTETLEK 360
DB 325 DLPSLAADVESKDVCKNYAEAKDVLGMFLYETARRHPDYSVLLLRLLAKTYTETLEK 384
QY 361 CAAADPHECYAKVDFEKLPIVEEPQNLIKONCELFQOLGEYKQNALLYRYTKVQVST 420
DB 385 CATDDPPTCYAKVDFEKLPIVEEPQNLIKONCELFQOLGEYKQNALLYRYTKVQVST 444
QY 421 PTLVEVSRNLGKVGSKCKKHPAKRMPCAEDYLSVVLNOLCVLHETKTPVSDRYTKCTES 480
DB 445 PTLVEVSRNLGKVGSKCKKHPAKRMPCAEDYLSVVLNOLCVLHETKTPVSDRYTKCTES 504
QY 481 LVNRRPCFSALEVDEYTPVPEKFAETFTFHADICTLSERQIKKOTALVELVKKPKAT 540

Db 505 LVNRPCFSGLEVDVETVPKFEAETFTFHADLCTLPEAEKQVKKOTALVELLKHKPKAT 564
QY 541 KEOLKAVMDFFAFAVEKCKADKQETCFAEKGLKVAASQAAL 583
Db 565 DEQLKTVMGDFGAFVEKCAAEKKEGCFSEEGPKLVNAQAAL 607
RESULT 5
ID ALBU_HORSE STANDARD; PRT; 607 AA.
AC P35747;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=93345495; PubMed=8344282;
RA Ho J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;
RT "X-ray and primary structure of horse serum albumin (Equus caballus)
at 0.27-nm resolution."
RL Eur. J. Biochem. 215:205-212(1993).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74045; CAA52194.1; -
CC PIR; S34053; ABOS.
CC HSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; P00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 594 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT METAL 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384

FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471
FT DISULFID 484 500
FT DISULFID 499 510
FT DISULFID 537 582
FT DISULFID 581 590
SQ SEQUENCE 607 AA; 68598 MW; 256F6E830A1B90C5 CRC64;
Query Match 79.8%; Score 2475.5; DB 1; Length 607;
Best Local Similarity 76.3%; Pred. No. 2.2e-154;
Matches 445; Conservative 69; Mismatches 68; Indels 1; Gaps 1;
QY 1 DAHKSEVAHRFKDGLGENFKALVIAFAOYLQOCPEFDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 DTHKSEIAHRFNDLGEKHFGLVAFSQYLQOCPEFDHVKLVNEVTEFAKCAADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCAKQEPERNECFLOHKDDNPNRLVRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCAKQEPERNECFLOHKDDNPNRLVRPEV 143
QY 121 DVMCTAFHNEETFLAKYLYEIAIRRHPIFYAPPELLLFAKRYKAAFTCCCAADKAACLLP 180
Db 144 DAQCAAFQEDPDKFLGYLYEVARRHPIFYGPELLLFAEYKADFTCCCPADKLAELIP 203
QY 181 KLDELDEGKASSAKORLKCASIQKGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK 240
Db 204 KLDALKEKILLSSAKERLKCSSQFNGERAVKANSVARLSQKPKADFAEVSKIYDLDTK 263
QY 241 VHTCCGDLLECCADRADLAKYICENQDISISLKECCCKPILLEKSHCIAEVENDEMPA 300
Db 264 VHKCCGDLLECCADRADLAKYICENQDISISLKECCCKPILLEKSHCIAEVEDDLP 323
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEYARRHPDYSVVLRLAKTVEETLEK 360
Db 324 DLPALAADFAEDKEICKYKDAKDFLGTFLYYSRRHPDYSVSLRLIAKTYEATLEK 383
QY 361 CAAADPEHYKAVDFEFKPLVEPQNLINQCELFQQLGKQFNALLVRYTKKVPQVST 420
Db 384 CAEADPPACYRTVDFQFTPLVEEPKSLVKNKCNDFEEVGEYDFQNALIVRYTKKAPQVST 443
QY 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVLNQLCVLHEKTPYSDRVTKCCTES 480
Db 444 PTLVEIGRTLGVKVGSRCKCLPESELRPCSENHLALNRLCVLHEKTPYSEKTKCCTDS 503
QY 481 LVNRPCFSALEVDVETVPKFEAETFTFHADICTLSEKERQIKKQTALVELLKHKPKAT 540
Db 504 LAERPCFSALELDEGVKPEKAEFTFHADICTLPEDEKQIKKQSALAEVLKHKPKAT 563
QY 541 KEOLKAVMDFFAFAVEKCKADKQETCFAEKGLKVAASQAAL 583
Db 564 KEOLKTVLGNFSAFAVAKCGREDKEACFAEAGPKLVASSQAAL 606
RESULT 6
ID ALBU_BOVIN STANDARD; PRT; 607 AA.
AC P02769; O02787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Bos d 6).
GN ALB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Holowachuk E.W., Stoltzenberg J.K., Reed R.G., Peters T. Jr.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Barry T., Power S., Gannon F.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-32.
 RX MEDLINE=80024278; PubMed=488109;
 RA McGilivray R.T.A., Chung D.W., Davie E.W.;
 RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of prealbumin."
 RL Eur. J. Biochem. 98:477-485(1979).
 RN [5]
 RP SEQUENCE OF 25-424 AND 429-607.
 RA Brown J.R.;
 RT "Structure of bovine serum albumin."
 RL Fed. Proc. 34:591-591(1975).
 RN [6]
 RP REVISIONS TO 190-195.
 RA Brown J.R.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [7]
 RP SEQUENCE OF 402-433.
 RX MEDLINE=82023364; PubMed=7283978;
 RA Reed R.G., Putnam F.W., Peters T. Jr.;
 RT "Sequence of residues 400-403 of bovine serum albumin."
 RL Biochem. J. 191:867-868(1980).
 RN [8]
 RP SEQUENCE OF 19-28.
 RX MEDLINE=77134075; PubMed=843354;
 RA Patterson J.E., Geller D.M.;
 RT "Bovine microsomal albumin: amino terminal sequence of bovine prealbumin."
 RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
 RN [9]
 RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.
 RX MEDLINE=91083649; PubMed=2260975;
 RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
 RT "Rapid confirmation and revision of the primary structure of bovine serum albumin by ES/MS and Frit-FAB LC/MS."
 RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
 RN [10]
 RP SEQUENCE OF 25-41.
 RX MEDLINE=88267456; PubMed=3389500;
 RA Hsieh J.C., Lin F.P., Tam M.F.;
 RT "Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing."
 RL Anal. Biochem. 170:1-8(1988).
 RN [11]
 RP SEQUENCE OF 437-451.
 RA Vilbois F.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 RN [12]
 RP DISULFIDE BONDS.
 RA Brown J.R.;
 RT "Structure of serum albumin: disulfide bridges."
 RL Fed. Proc. 33:1389-1389(1974).
 CC -|- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA. HAS A GOOD BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: PLASMA.
 CC -|- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -|- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M73993; AAA51411.1; -;
 DR EMBL; X58989; CAA41735.1; -;
 DR EMBL; Y17769; CAA76847.1; -;
 DR PIR; A38885; ABBOS.
 DR HSSP; P02768; 1E7B.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PO0802; SERUMALBUMIN.
 DR PRODOM; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Plasma; Albumin; Metal-binding; Lipid-binding; Repeat; Signal;
 KW Copper; Allergen.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 607 SERUM ALBUMIN.
 FT DOMAIN 25 204 ALBUMIN 1.
 FT DOMAIN 211 396 ALBUMIN 2.
 FT DOMAIN 403 594 ALBUMIN 3.
 FT METAL 27 27 COPPER (BY SIMILARITY).
 FT DISULFID 77 86
 FT DISULFID 99 115
 FT DISULFID 114 125
 FT DISULFID 147 192
 FT DISULFID 191 200
 FT DISULFID 223 269
 FT DISULFID 268 276
 FT DISULFID 288 302
 FT DISULFID 301 312
 FT DISULFID 339 384
 FT DISULFID 383 392
 FT DISULFID 415 461
 FT DISULFID 460 471
 FT DISULFID 484 500
 FT DISULFID 499 510
 FT DISULFID 537 582
 FT DISULFID 581 590
 FT CONFLICT 214 214
 FT CONFLICT 302 302
 FT CONFLICT 304 305
 FT CONFLICT 324 324
 FT CONFLICT 394 395
 FT CONFLICT 437 437
 FT CONFLICT 493 494
 FT SEQUENCE 607 AA; 69293 MW; 39167DFE768585D4 CRC64;
 SQ
 Query Match 79.0%; Score 2450.5; DB 1; Length 607;
 Best Local Similarity 75.8%; Pred. No. 9.4e-153;
 Matches 442; Conservative 71; Mismatches 69; Indels 1; Gaps 1;
 Qy 1 DAHKSEVAHREFKDLGNEFKALVLIAPFAQYLOQCFFEDHVKLVNVEVTFEAKTCVADESAAE 60
 Db 25 DTHKSEIAHREFKDLGNEHFKGLVLIAPFAQYLOQCFFEDHVKLVNVEVTFEAKTCVADESAAE 84
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPILRLVPRPEV 120
 Db 85 GCEKSLHTLFGDELCKVASLRETYGDMADCCQEPERNECFLSHKDDSPDLPKL-KPDP 143
 Qy 121 DVMCTAFHNDNEETFLUKKLYEIAIRHPHYFAPPELLFFAKRYKAAFTCCQAADKACLLP 180
 Db 144 NTLCDDEFKADKKWKGKLYEIAIRHPHYFAPPELLYYANKYVGFQECQCAEDKACLLP 203
 Qy 181 KLDELDFEGKASSAKQRLKCSAQKQFGRAPKAWAVARLSQRPKAEVSKLVTDLTK 240
 Db 204 KIETNRKVLASSAKQRLKCSAQKQFGRAPKAWAVARLSQRPKAEVSKLVTDLTK 263
 Qy 241 VHTCCCHGDLLECADRADLAKYICENQDISSKLKECKECPLEKSHCIAEVENDEMPA 300

Db 264 VHKCECHGDLLECCADRADLAKVTCNDQDTISSKLEKCCDKPLLEKSHCAEVEKDAIPE 323
QY 301 DLPSLAADFVESKDVCKNYAEADKVLGMLFYEARHPDYSVVLLRLAKTETTTLEKC 360
Db 324 NLPLTDAFADKDKVCKNYQKDAFGLSFLYERHPEYAVSVLLRLAKYEATLEEC 383
QY 361 CAADAPHECYAKVDFEKPVEPQNLKQNCDFEOLGKQFQNLALVRYTKKPOVST 420
Db 384 CAKDDPHACVSTVEDKHLVDEPQNLKQNCDFEOLGKQFQNLALVRYTKKPOVST 443
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
Db 444 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSEKVTCKCTES 503
QY 481 LVNRRCFSALEVDEYVVPKEFNAETFFHADICTLSEKERQIKKQATLVLLVKKHKKPKAT 540
Db 504 LVNRRCFSALEVDEYVVPKEFNAETFFHADICTLSEKERQIKKQATLVLLVKKHKKPKAT 563
QY 541 KEOLKAVMDFAAFVEKCKCKADKDKETCFABEGKKLVAAASQAL 583
Db 564 EEQLKTVWENFVAFVCKCAADKDEACFAVEGPKLVVSTQAL 606

RESULT 7
ALBU_RABIT STANDARD; PRT; 608 AA.
AC P49065;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-New Zealand white; TISSUE=Liver;
RA Sheffield W.P., Syed S., Schuyler P.D.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. Usage by and for commercial
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18344; AAB58347.1; -;
DR HSSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.

FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 96 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
SQ SEQUENCE 608 AA; 68914 MW; CF5E92647AAFE9A2 CRC64;
Query Match 78.8%; Score 2446; DB 1; Length 608;
Best Local Similarity 74.1%; Pred. No. 1.9e-152;
Matches 433; Conservative 77; Mismatches 74; Indels 0; Gaps 0;
QY 1 DAHKSEVAFHFKDGLGENFKALVIAFAOYLQCCPDHVKLVNEVTEFAKTCVADESAAE 60
Db 25 EAHKSEIAHFRNDVGEHFGLVITFSQYLQKCPVEEHAKLVKEVTDLAKACVADESAA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEKPERNECFLOHKDDNPNLRLVRPE 120
Db 85 NCDKSLHDFGDKICALPSLRTDYGVADCCCKEKEPERNECFLOHKDDNPNLRLVRPE 144
QY 121 DVMCTAFHNEETFLAKLYEIAARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 145 DVLKAFPHDDEKAFGHYLYEVARHPYFYAPPELLFYAOKYKAILTECCQAADKAACLLP 204
QY 181 KLDELDEGKASAKORLKCAKQKGERAFKAWARLARSORFPKAEFAVSVKLVTDLTK 240
Db 205 KLDALSGKSLISAQERLRCASIQKFGDRAYKAWALVLSORFPKADFTDISKIVTDLTK 264
QY 241 VHTCECHGDLLECCADRADLAKYICENQDSISSKLEKCCDKPLLEKSHCAEVEKDAIPE 300
Db 265 VHKCECHGDLLECCADRADLAKYICENQDSISSKLEKCCDKPLLEKSHCAEVEKDAIPE 324
QY 301 DLPSLAADFVESKDVCKNYAEADKVLGMLFYEARHPDYSVVLLRLAKTETTTLEKC 360
Db 325 GLPAVAEEFVEDKDVCKNYEAEKDLFLGKFLYERHPEYAVSVVLLRLAKYEATLEEC 384
QY 361 CAADAPHECYAKVDFEKPVEPQNLKQNCDFEOLGKQFQNLALVRYTKKPOVST 420
Db 385 CATDDPHACVSTVEDKHLVDEPQNLKQNCDFEOLGKQFQNLALVRYTKKPOVST 444
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
Db 445 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSEKVTCKCTES 504
QY 481 LVNRRCFSALEVDEYVVPKEFNAETFFHADICTLSEKERQIKKQATLVLLVKKHKKPKAT 540
Db 505 LVNRRCFSALEVDEYVVPKEFNAETFFHADICTLSEKERQIKKQATLVLLVKKHKKPKAT 564
QY 541 KEOLKAVMDFAAFVEKCKCKADKDKETCFABEGKKLVAAASQALG 584
Db 565 NDQLKTVWGEFTALLDKCCSAEDKEACFAVEGPKLVVSTQALG 608
RESULT 8
ALBU_SHEEP
ID ALBU_SHEEP STANDARD; PRT; 607 AA.
AC P14639;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)

RT bromide cleavage of rat serum albumin.";

RL J. Biochem. 83:35-48(1978).

RN [4]

RP SEQUENCE OF 223-288 AND 572-608.

RA MEDLINE=76260153; PubMed=956149;

RX Isemura S., Ikenaka T.;

RT "Fragmentation of rat serum albumin by cyanogen bromide cleavage and

RT the amino acid sequences of four fragments.";

RL J. Biochem. 79:1183-1196(1976).

RN [5]

RP SEQUENCE OF 166-174.

RC TISSUE=Plasma;

RX MEDLINE=87194805; PubMed=2437111;

RA Carraway R.E., Mitra S.P., Cochrane D.E.;

RT "Structure of a biologically active neurotensin-related peptide

RT obtained from pepsin-treated albumin(s).";

RL J. Biol. Chem. 262:5968-5973(1987).

RN [6]

RP COPPER-BINDING.

RX MEDLINE=79001617; PubMed=80265;

RA Aoyagi Y., Ikenaka T., Ichida F.;

RT "Copper(II)-binding ability of human alpha-fetoprotein.";

RL Cancer Res. 38:3483-3486(1978).

CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD

CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,

CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE

CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.

CC -1- FUNCTION: NRP REGULATES FAT DIGESTION, LIPID ABSORPTION, AND

CC BLOOD FLOW (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.

CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; V01222; CAA24532.1; -;

DR PIR; A03233; ABRTS.

DR HSP; P02768; IE7B.

DR InterPro: IPR000264; Serum_albumin.

DR Pfam; PF00273; transport_prot; 3.

DR PRINTS; PR00802; SERUMALBUMIN.

DR PRODOM; PD002486; Serum_albumin.

DR SMART; SM00103; ALBUMIN; 3.

DR PROSITE; PS00212; ALBUMIN; 3.

KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;

KW Copper.

FT SIGNAL 1 18

FT PROPEP 19 24

FT CHAIN 25 608

FT PEPTIDE 166 174

FT DOMAIN 25 205

FT DOMAIN 212 397

FT DOMAIN 404 595

FT METAL 27 27

FT DISULFID 77 86

FT DISULFID 99 115

FT DISULFID 114 125

FT DISULFID 148 193

FT DISULFID 192 201

FT DISULFID 224 270

FT DISULFID 269 277

FT DISULFID 289 303

FT DISULFID 302 313

FT DISULFID 340 385

FT DISULFID 384 393

FT DISULFID 416 462

FT SERUM ALBUMIN.

FT NEUTROTENSIN-RELATED PEPTIDE.

FT ALBUMIN 1.

FT ALBUMIN 2.

FT ALBUMIN 3.

FT COPPER.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT DISULFID 461 472 BY SIMILARITY.

FT DISULFID 485 501 BY SIMILARITY.

FT DISULFID 500 511 BY SIMILARITY.

FT DISULFID 538 583 BY SIMILARITY.

FT DISULFID 582 591 BY SIMILARITY.

FT VARIANT 262 262 V -> L.

FT CONFLICT 174 174 Y -> L (IN REF. 5).

SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;

Query Match 78.2%; Score 2426; DB 1; Length 608;

Best Local Similarity 73.4%; Pred. No. 3.7e-151;

Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;

QY 1 DAHKSEVAHFKDLGEENFKALVIAFAOYLQCCPFEDHVKLVNEVTEFAKTCVADSAE 60

DB 25 EAHKSEIAHFKDLGEHFKGLVLIASFQYLQCKPYEHKLVQEVTFDAKTCVADENAE 84

QY 61 NCDKSLHTLFEGDKLCTVATLRETYGEMADCCAKOEPRNECFLOHKDDNPNLPLVPEV 120

DB 85 NCDKSIHTLFEGDKLCAIPKLRDNYGELADCCAKOEPRNECFLOHKDDNPNLPPQPEA 144

QY 121 DVNCTAFHNEETFLKKLYEIAHRRHPFYAPPELLFFAKRYKAAFTTECCOAAADKAACLLP 180

DB 145 EAMCTSEFNPTFLGHYHEVARHHPFYAPPELLLYAERYNEVLTQCCSTESDKAACLT 204

QY 181 KLDELREGKASSAKORLKCAQLQKGFERAFKAWAVARLSORPPKAEFAEYVKLVTLDTK 240

DB 205 KLDVKEKALVAVRQRMKSSMORGERAFKAWAVARMSORPNAEFAITKLATDVTK 264

QY 241 VHTCCCHGDLLECCADDRADLAKYICENQDSISSKLECEKPLEKSHCIAEVENDEMPA 300

DB 265 INKECCHGDLLECCADDRADLAKYICENQATISSKLOACCDKPVQLKSOCLAEETHDNIPA 324

QY 301 DLPSLADEFESKDVCKNYAEAKDVLGMLFELYEARHPOYSVVLRLAKTAYETTLK 360

DB 325 DLPSIAADFEDKEVCKNYAEAKDVLGTLFELYESSRHPDYSVLLRLAKKYEATLEK 384

QY 361 CAAADHECVAKYDFEKLVEPQNLKONCELFQGLGEYKFNALLVRYTKVPOVST 420

DB 385 CAGSDPPACVGTVLAEEQPLVEEPKLVKTNCELYEKLGEYQNAVLYRYTKAPOVST 444

QY 421 PTLVEVSRNLGVSGKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

DB 445 PTLVEAARNLGRVGTCKCTLPEAORLPCVEDYLSAILNRLCVLHEKTPVSEKVTCKCSGS 504

QY 481 LVNRRPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKQTALVELYKHKPKAT 540

DB 505 LVERRPCFSALTVDETYVPKEFNAETFFHSDICTLTPDKEKQIKQTALAEVLKHKPKAT 564

QY 541 KEOLKAVMDDFAAFEKCKCKADDKCTCFAEEGKKLVAAASQAL 583

DB 565 EDQLKTVMGDFQFVDKCKCKADKDNCFATEGPNLVARSREAL 607

RESULT 10

ALBU_PIG STANDARD; PRT; 605 AA.

ID ALBU_PIG Q29018;

AC P08835; Q29018; (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Serum albumin precursor (Fragment).

GN ALB.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89016582; PubMed=3174440;

RA Baldwin G.S., Weinstein J.;

RT "Nucleotide sequence of porcine liver albumin.";

DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SMO0103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
 KW Copper.

FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 BY SIMILARITY.
 FT CHAIN 25 609 SERUM ALBUMIN.
 FT DOMAIN 25 206 ALBUMIN 1.
 FT DOMAIN 213 398 ALBUMIN 2.
 FT DOMAIN 405 596 ALBUMIN 3.
 FT METAL 28 28 COPPER.
 FT DISULFID 78 87 BY SIMILARITY.
 FT DISULFID 100 116 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 149 194 BY SIMILARITY.
 FT DISULFID 193 202 BY SIMILARITY.
 FT DISULFID 225 271 BY SIMILARITY.
 FT DISULFID 270 278 BY SIMILARITY.
 FT DISULFID 290 304 BY SIMILARITY.
 FT DISULFID 303 314 BY SIMILARITY.
 FT DISULFID 341 386 BY SIMILARITY.
 FT DISULFID 385 394 BY SIMILARITY.
 FT DISULFID 417 463 BY SIMILARITY.
 FT DISULFID 462 473 BY SIMILARITY.
 FT DISULFID 486 502 BY SIMILARITY.
 FT DISULFID 501 512 BY SIMILARITY.
 FT DISULFID 539 584 BY SIMILARITY.
 FT DISULFID 583 592 BY SIMILARITY.
 SQ SEQUENCE 609 AA; 68940 MW; 9CA5F97F67EF1A48 CRC64;
 Query Match 76.9%; Score 2387; DB 1; Length 609;
 Best Local Similarity 73.9%; Pred. No. 1.3e-148;
 Matches 430; Conservative 65; Mismatches 87; Indels 0; Gaps 0;
 QY 2 AHKSEVAHFKDGEENFKALVIAFYAQYLOQCPFFEDHVKLVNEVTEFAKTCVADESAEN 61
 DB 27 AHKSEIAHRYKDLGKYEYKGLVLYTFQYLOKCSYEHVKLVREVTDFASNAKDESAEN 86
 QY 62 CDKSLHPTLFGDKLCTVATLRETGEMADCCAKQEPERNECFLOHKDNDPNLPLRVPEVD 121
 DB 87 CDKSLHPTLFGDKLCTVATLRETGEMADCCAKQEPERNECFLOHKDNDPNLPLRVPEVD 146
 QY 122 VMCTAFHNEETFLKYLVIATRRHPFYFAPPELLFPAKRYKAAFTCCQAADKAACLLPK 181
 DB 147 AMCTAFQENAEAFMGHLYHEVARRHPFYCGPELLYADKYAVLTCCAADKGACILTPK 206
 QY 182 LDELRDGKASSAKQRLKASLOKFGRAKNAVARLSORFPAEYVSKLVTDITKV 241
 DB 207 LDALKERKALVSARQRLKCSMKKFGRAKNAVARMSOTFPNADPAETTKLATDLTKV 266
 QY 242 HTECCHGDLLECADDRLAKYICENODSTSSKLKCECKPPLKSHCIAEVENDEMPAD 301
 DB 267 TQECCHGDLLECADDRLAKYICENODSTSSKLQACCKREMLQKSOCLAEVEHDDMPAD 326
 QY 302 LPSLAADFVESKDVCKNYAEAKDVFGLMGFLYEARHPDYSVVLRLAKLYETTTLEKCC 361
 DB 327 LPALTADVEDKDVCKNYAEAKDVFGLMGFLYEARHPDYSVVLRLAKLYETTTLEKCC 386
 QY 362 AADPHCEYAKVDFDEKPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVQVSTP 421
 DB 387 AADPHCEYAKVDFDEKPLVEEPQNLKQNCLEFQELGEYKFNALLVRYTKVQVSTP 446
 QY 422 TLVEVSRLKGVSKCKHPKAEKRMPCAEYDLSVVLNQLCVLHEKTPVSDRVTKCCTESL 481
 DB 447 TLVEAARSLGRVTHCCALPEKRLPCVEDYLSAILNRVCLLHEKTPVSDRVTKCCTESL 506
 QY 482 VNRPPCFSALEVDYVYPKEAFNAETFTFHADICTLSEKERQIKQATLALVELVKKPKATK 541
 DB 507 VERRPPCFSALEVDYVYPKEAFNAETFTFHADICTLSEKERQIKQATLALVELVKKPKATK 566
 QY 542 EQLKAYMDDFAAFVCKCKADDDTCAEFGKLVAAASQAL 583

Db 567 EQLKVKMGDFAEFLEKCKQEDKEACFSTEGPKLVAESQAL 608
 RESULT 12
 ALBU_MOUSE STANDARD; PRT; 608 AA.
 AC P07724; Q61802;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB OR ALBI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Hono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE OF 99-516 FROM N.A..
 RX MEDLINE=88216123; PubMed=2452956;
 RA Minghetti P.P., Law S.W., Dugaiczky A.;
 RT "The rate of molecular evolution of alpha-fetoprotein approaches that
 of pseudogenes.";
 RL Mol. Biol. Evol. 2:347-358(1985).
 RN [4]
 RP SEQUENCE OF 477-551 FROM N.A..
 RC STRAIN=BALB/C;
 RX MEDLINE=90269606; PubMed=1971802;
 RA Boccardo C., Deschattrette J., Meunier-Rotival M.;
 RT "Empty and occupied insertion site of the truncated LINE-1 repeat
 located in the mouse serum albumin-encoding gene.";
 RL Gene 88:181-186(1990).
 RN [5]
 RP SEQUENCE OF 25-44.
 RC TISSUE=Liver;
 RX MEDLINE=93162044; PubMed=1286668;
 RA Glometti C.S., Taylor J., Tollaksen S.L.;
 RT "Mouse liver protein database: a catalog of proteins detected by two-
 dimensional gel electrophoresis.";
 RL Electrophoresis 13:970-991(1992).
 CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
 BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -|- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AJ011413; CAA09617.1; -
DR EMBL; M16111; AAA37190.1; -
DR EMBL; X13060; CAA31458.1; -
DR EMBL; AK010025; BAB26650.1; -
DR PIR; A05139; A05139.
DR HSSP; P02768; IE7B.
DR SWISS-2DPAGE; P07724; MOUSE.
DR MGI; MGI:87991; Albi.
DR InterPro; IPR00264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CONFLICT 27 27 H -> D (IN REF. 5).
FT CONFLICT 33 33 H -> D (IN REF. 5).
FT CONFLICT 41 41 Q -> I (IN REF. 5).
SQ SEQUENCE 608 AA; 68692 MW; 292F7C7EED3A61B4 CRC64;

Query Match 76.6%; Score 2378; DB 1; Length 608;
Best Local Similarity 72.4%; Pred. No. 5e-148;
Matches 422; Conservative 80; Mismatches 81; Indels 0; Gaps 0;
Oy 1 DAHKEVAHRKFDLGEENFKALVIAFAQYLQOCFFEDHVKLVNVEFAKTCVADESAA 60
Db 25 EAHKSEIHRNDLGEQFKGLVIAFAQYLQOCFFEDHVKLVNVEFAKTCVADESAA 84
Oy 61 NCDKSLHFLGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNPMLPRVREPV 120
Db 85 NCDKSLHFLGDKLCAIPNLRENYGELADCCQKQPERNECFLOHKDNPMLPRVREPV 144
Oy 121 DVNCTAFHNDNEFTLUKKYIETARRHPYFYAPPELLFFAKRYKAAFTCCQADKAACLLP 180
Db 145 EAMCTSFKENPTTFMGHYLHEVARHPYFYAPPELLFYAEQYNEILLTQCCAEADKESCLTP 204

Oy 181 KLDELDRDEGKASSAKQRLKCSAQKQFGERAFKAVARLSQRFKAEFAEYKSLVDTLTK 240
Db 205 KLDGVKEKALVSSVQRMKCSMQKQFGERAFKAVARLSQTFPNADFAETKLTATLTK 264
Oy 241 VHTECCHGDLLECADRADLAKYICENODSISSSKLUKCEKPLLEKSHCIAEVENDEMPA 300
Db 265 VNKECCCHGDLLECADRADLAKYICENQATISSKLTQCCDKPLKKAHCLSEVEHDTMPA 324
Oy 301 DLPSLAADFEVSKDCKNYAKADVFLGMFLYEVARRHPDYVSVLLLRLLAKTYETLEK 360
Db 325 DLPAIAADFEVDEQEVKNYAKADVFLGFLYEVARRHPDYVSVLLLRLLAKTYETLEK 384
Oy 361 CAAADPHCEYAKVDFEFPKPLVEEPQNLKQNCLEFQELGKQFQNALVVRVTKKPVQYST 420
Db 385 CAENPPACYCTVLAEFQPLVEEPKLVKTYNCDLYELGKQFQNALVVRVTKKPVQYST 444
Oy 421 PTLVEVSRNLKGVSKCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEAARNLGRVGTCKCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGS 504
Oy 481 LVNRRPCFSALEVDVYVPKFNATFTFHADICTLSKEKQIKKOTALVELVHKHPRAT 540
Db 505 LVNRRPCFSALEVDVYVPKFNATFTFHADICTLSKEKQIKKOTALVELVHKHPRAT 564
Oy 541 KEQLKAVMDFAAFVEKCKKADDETCTFAEEGKKLVAASQAAL 583
Db 565 AEQLKTVMDFAAQFLDTCCKAADKDTCTFSTEGPNLVTRCKDAL 607

RESULT 13
ALBU_CHICK STANDARD; PRT; 615 AA.
AC P19121:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cassidy A.I., Salkilid C.K., Baverstock P., Wallace J.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=83161037; PubMed=6187737;
RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
RT "The 5' noncoding and flanking regions of the avian very low density
RT apolipoprotein II and serum albumin genes. Homologies with the egg
RT white protein genes."
RL J. Biol. Chem. 258:4556-4564(1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE=78019943; PubMed=911327;
RA Rosen A.M., Geller D.M.;
RT "Chicken microsomal albumin: amino terminal sequence of chicken
RT proalbumin."
RL Biochem. Biophys. Res. Commun. 78:1060-1066(1977).
CC -|- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -|- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

FT	DOMAIN	212	397	ALBUMIN 2.
FT	DOMAIN	404	595	ALBUMIN 3.
FT	METAL	22	22	COPPER AND NICKEL (BY SIMILARITY).
FT	DISULFID	99	114	BY SIMILARITY.
FT	DISULFID	113	124	BY SIMILARITY.
FT	DISULFID	148	193	BY SIMILARITY.
FT	DISULFID	192	201	BY SIMILARITY.
FT	DISULFID	224	270	BY SIMILARITY.
FT	DISULFID	269	277	BY SIMILARITY.
FT	DISULFID	289	303	BY SIMILARITY.
FT	DISULFID	302	313	BY SIMILARITY.
FT	DISULFID	384	393	BY SIMILARITY.
FT	DISULFID	416	462	BY SIMILARITY.
FT	DISULFID	461	472	BY SIMILARITY.
FT	DISULFID	485	501	BY SIMILARITY.
FT	DISULFID	500	511	BY SIMILARITY.
FT	DISULFID	538	583	BY SIMILARITY.
FT	DISULFID	582	591	BY SIMILARITY.
FT	CARBOHYD	42	42	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	609 AA; 68741 MW;	C032987CAD0E672B	CRC64;

Query Match

Best Local Similarity

Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

40.4%; Score 1253.5; DB 1; Length 609;

40.1%; Pred. No. 1.1e-74;

QY	3	HKSE-----VAHRPKDLGEENFKALVLI	FAFAVLOQCPQFEDHVKLVN	TEVTEFAKTCVADE	57
DB	22	HRNEYGIASILDSYCTAEINLTDLTI	FFAQVQVQATYKVEVSKVWKDALTAEK	PTGDE	81
QY	58	SAENCKSLHTLFGDKLCTVATLRETY	GEMADCCAKOPEPERNECFQLQHKDDNP	-NLPLRV	116
DB	82	QSAGCLENQLPAFLEELCREKEILEKYGH	-SDCCSQSEGRHNCFLAHKKTPTASIPFQ	140	
QY	117	RPEVDMVCTAFHDNEETFLKLYETARR	HPYFAPPELLFFAKRYKAAFTCCQAAADKAA	176	
DB	141	VPEPVTSCAEYEDRETFMKNFTIETARR	HPFLYAPFTILLWAARYDKIPTSCCKAENAVE	200	
QY	177	CLLPKLELDRDEGKASSAKORUKCASLO	KQFGERAFKAWAVARLSORFPKRAEFAEVSKLYT	236	
DB	201	CFOTKAAATVTKEURSSLLNQHACAVMKN	FGTRTFOAITVKLSQKFTKVNFTFIOKLVL	260	
QY	237	DLTKVHTECCGHDLLCADDRADLAKYIC	ENQDSISSKLEKCECEKPLLEKSHCIAEVEND	296	
DB	261	DVAHVHECHCRGVDLCLQDGEKIMYSIC	QDDTFLSNKITECCKLTLRGGQCIHAEND	320	
QY	297	EMPADLPALADPESKVCKNVAEKDVLGM	FLFYARRHPDYSVLLLRLLAKTYETT	356	
DB	321	EKPEGLSNLNRFLGDRDFNQFSSGKRNIF	LASFVHEYSRRHPQLAVSVILRVAKGYQEL	380	
QY	357	LEKCCAAADPHECYAKVDFEFLPVEBPON	LKQNCLEFOLGEYKFPQNALLVRYTKVP	416	
DB	381	LEKCFQTEPNLECODKGBEELQYIQESAL	AKRSGLGFQKGEYLYQNALFVAYTKKAP	440	
QY	417	QVSTPTLVEVSRNLGVSKCKHPEAKR	MPCAEDYLSVVLNOLCVLHEKTPVSDRVTKC	476	
DB	441	QLTSSSELMATRKNWATAATCCQLSEDKL	LACGEGAADIIGHLICIRHETTPNPGVGQC	500	
QY	477	CTESLVNRPCFSALEVDITYVPKNEAET	FTPHADICLSEKEROIKOTALVELVKKH	536	
DB	501	CTSSYANRRPCFSSLVVDITYVPAFSDDK	FIHKDLCQAQGVALQTMKQEFNLVLVKQK	560	
QY	537	PKATKEOLKAVMDFAFAFVEKCKADKDE	KYCFAEEGKKLVAAQOALGL	585	
DB	561	POITEQLEAVIADPFSGLLEKCCQGGEQE	VCFAEEGOKLISKTRAAALGV	609	

RESULT 15

FETA_HUMAN

ID FETA_HUMAN

STANDARD; PRT; 609 AA.

AC P02771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein).
GN	AFP.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=83273664; PubMed=6192439;
RA	Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
RT	"Primary structures of human alpha-fetoprotein and its mRNA.";
RL	Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=87185438; PubMed=2436661;
RA	Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczak A.;
RT	"Structure, polymorphism, and novel repeated DNA elements revealed by a complete sequence of the human alpha-fetoprotein gene.";
RL	Biochemistry 26:1332-1343(1987).
RN	[3]
RP	SEQUENCE OF 1-28 FROM N.A.
RX	MEDLINE=93278385; PubMed=7684942;
RA	Mcvey J.H., Michaelides K., Hansen L.P., Ferguson-Smith M.,
RA	Tilghman S., Krumlauf R., Tuddenham E.G.D.;
RT	"A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gene is associated with hereditary persistence of alpha-fetoprotein (HPAFP).";
RL	Hum. Mol. Genet. 2:379-379(1993).
RN	[4]
RP	SEQUENCE OF 429-556 FROM N.A.
RX	MEDLINE=83158778; PubMed=6187626;
RA	Beattie W.G., Dugaiczak A.;
RT	"Structure and evolution of human alpha-fetoprotein deduced from partial sequence of cloned cDNA.";
RL	Gene 20:415-422(1982).
RN	[5]
RP	PARTIAL SEQUENCE OF 19-609.
RX	MEDLINE=91242409; PubMed=1709810;
RA	Pucci P., Siciliano R., Malorni A., Marino G., Tecce M.F.,
RA	Ceccarini C., Terrana B.;
RT	"Human alpha-fetoprotein primary structure: a mass spectrometric study.";
RL	Biochemistry 30:5061-5066(1991).
RN	[6]
RP	PRELIMINARY SEQUENCE OF 19-35.
RX	MEDLINE=77242506; PubMed=70228;
RA	Yachnin S., Hsu R., Heinrichson R.L., Miller J.B.;
RT	"Studies on human alpha-fetoprotein. Isolation and characterization of monomeric and polymeric forms and amino-terminal sequence analysis.";
RL	Biochim. Biophys. Acta 493:418-428(1977).
RN	[7]
RP	PRELIMINARY SEQUENCE OF 19-38.
RX	MEDLINE=78001760; PubMed=711198;
RA	Aoyagi Y., Ikenaka T., Ichida F.;
RT	"Comparative chemical structures of human alpha-fetoproteins from fetal serum and from ascites fluid of a patient with hepatoma.";
RL	Cancer Res. 37:3663-3667(1977).
RN	[8]
RP	PRELIMINARY SEQUENCE OF 19-39.
RX	MEDLINE=75018719; PubMed=4138095;
RA	Ruostelahti E., Pihko H., Vaheri A., Seppala M., Virolainen M.,
RA	Kontinen A.;
RT	"Alpha fetoprotein: structure and expression in man and inbred mouse strains under normal conditions and liver injury.";
RL	Johns Hopkins Med. J. Suppl. 3:249-255(1974).
RN	[9]
RP	GENE STRUCTURE.
RX	MEDLINE=85182629; PubMed=2580830;
RA	Sakai M., Morinaga T., Urano Y., Watanabe K., Wegmann T.G.,
RA	Tamaoki T.;

RT "The human alpha-fetoprotein gene. Sequence organization and the 5' flanking region.";
 RL J. Biol. Chem. 260:5055-5060(1985).
 RN [10]
 RP METAL-BINDING.
 RX MEDLINE-79001617; PubMed-80265;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Copper(II)-binding ability of human alpha-fetoprotein.";
 RL Cancer Res. 38:3483-3486(1978).
 RN [11]
 RP BILIRUBIN-BINDING.
 RX MEDLINE-80001710; PubMed-89900;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding ability.";
 RL Cancer Res. 39:3571-3574(1979).
 RN [12]
 RP SULFATION.
 RX MEDLINE-86042625; PubMed-2414772;
 RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line HepG2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 CC -1- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND BILIRUBIN LESS WELL THAN, SERUM ALBUMIN. ONLY A SMALL PERCENTAGE (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES.
 CC -1- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION TO THE MONOMERIC FORM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PLASMA. SYNTHESIZED BY THE FETAL LIVER AND YOLK SAC.
 CC -1- DEVELOPMENTAL STAGE: OCCURS IN THE PLASMA OF FETUSES MORE THAN 4 WEEKS OLD, REACHES THE HIGHEST LEVELS DURING THE 12TH-16TH WEEK OF GESTATION, AND DROPS TO TRACE AMOUNTS AFTER BIRTH. THE SERUM LEVEL IN ADULTS IS USUALLY LESS THAN 40 NG/ML. AFP OCCURS ALSO AT HIGH LEVELS IN THE PLASMA AND ASCITIC FLUID OF ADULTS WITH HEPATOMA.
 CC -1- PTM: INDEPENDENT STUDIES SUGGEST HETEROGENEITY OF THE AMINO-TERMINAL SEQUENCE OF THE MATURE PROTEIN AND OF THE CLEAVAGE SITE OF THE SIGNAL SEQUENCE.
 CC -1- PTM: SULFATED.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M10949; AAA51674.1; -;
 DR EMBL; M10950; AAA51675.1; -;
 DR EMBL; V01514; CAA24758.1; -;
 DR EMBL; M16110; AAB58754.1; -;
 DR EMBL; Z19532; CAA79592.1; -;
 DR PIR; A03234; FPHU.
 DR PIR; A26624; A26624.
 DR HGSP; P02768; IE7B.
 DR GlycoSuiteDB; P02771; -;
 DR Sienra-2DPAGE; P02771; -;
 DR Genew; HGNC:317; AFP.
 DR MM; 104150; -;
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 2.
 DR GlycoProtein; Sulfation; Albumin; Plasma; Repeat; Metal-binding;
 KW Copper; Nickel; Signal; Polymorphism;
 FT SIGNAL 1 18
 FT CHAIN 19 609 ALPHA-FETOPROTEIN.

FT	DOMAIN	20	205	ALBUMIN 1.
FT	DOMAIN	212	397	ALBUMIN 2.
FT	DOMAIN	404	595	ALBUMIN 3.
FT	METAL	22	22	COPPER AND NICKEL.
FT	DISULFID	99	114	
FT	DISULFID	113	124	
FT	DISULFID	148	193	
FT	DISULFID	192	201	
FT	DISULFID	224	270	
FT	DISULFID	269	277	
FT	DISULFID	289	303	
FT	DISULFID	302	313	
FT	DISULFID	384	393	
FT	DISULFID	416	462	
FT	DISULFID	461	472	
FT	DISULFID	485	501	
FT	DISULFID	500	511	
FT	DISULFID	538	583	
FT	DISULFID	582	591	
FT	CARBOHYD	251	251	
FT	VARIANT	570	570	
FT	SEQUENCE	609 AA;	68677 MW;	4D4E45820E1C2D4F CRC64;
FT	SEQUENCE	609 AA;	68677 MW;	4D4E45820E1C2D4F CRC64;
FT	SEQUENCE	609 AA;	68677 MW;	4D4E45820E1C2D4F CRC64;

Query Match 40.3%; Score 1249.5; DB 1; Length 609;
 Best Local Similarity 39.9%; Pred. No. 1.9e-74;
 Matches 235; Conservative 116; Mismatches 231; Indels 7; Gaps 3;

QY	3	HKSE-----VAHRPKDLGEENFKALVLIAPAYIQQQPFEDHVKLVNVEVTEFAKTCVADE	57
DB	22	HRNEYGIASILDVSQTAETISLADLITFAQFVQEATYKEVSMVKVDALTAIEKPTGDE	81
QY	58	SAENCDKSLHTLFGDKLCTVATLRETGEMADCCAKOPEPNECFLOHKDDNP-NLRLV	116
DB	82	QSSCLENQLPAFLLELCEHEKEILEYGH-SDDCSQSEGRHNCFLAHKKFTPASIPLFQ	140
QY	117	RPEYDVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAA	176
DB	141	VPEPVTSCAEVEEDRETFMNKFIVEIARRHPFLVAPTILLWAARYDKTIPSCCKAENAVE	200
QY	177	CLLPKLDLDRDEGKASSAKQBLKCSAQKQGERAFKAWARLSQRPPKAFVSKLVT	236
DB	201	CFQTKAATVTYKELRESSLLNQHACAVMKNFGTRTFQAITVTKLSQKFTKVNFTIQKLV	260
QY	237	DLTKVHTCECHGDLLECADRADLAKYICENQDSISSKLKCECKPPLLEKSHCIAEVEND	296
DB	261	DVAIVHEHCGRGVLDCLQDGEKIMSYICSQODTSLNKHTECCCKLTTLERQCCLIHEND	320
QY	297	EMPADPLSLAADFVESKDVCKNYAEAKDVLGMLFLEYARRHPDYSVVLLRLAKTYETT	356
DB	321	EKPEGLSPNLNRLGDRDFNQFSSGKNIFLASPVHEYSRRHPQLAVSVILRVAKGYQEL	380
QY	357	LEKCCAADPHCEYAKVDFDEKPLVEEPQNLKONCELFQGEYKFNQALLVRYTKVP	416
DB	381	LEKCFOTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGYYLQNALVLAATYTKAP	440
QY	417	QVSTPTLVEYSRNLGKVGSKCKHPEAKRMPCAEDYLSVLNOLCVLHEKTPVSDRVTKC	476
DB	441	QLTSSELMAITRKMAATAATCCQLSEDKLLACGEGADIIIGHLCIRHMTVPVPGVQC	500
QY	477	CTESLVNRRRCFSALEVDETVVPKFEAFNAETFTFHADITLSEKERQIKQTALVELVKKH	536
DB	501	CTSSYANRRPCFSSLVVDVTVYVPAFSDDKFIFHKDLCAQGVVALQTMKQEFLLNLVKQ	560
QY	537	PKATKEQLKAVMDDFAAFEVKCKKADKCTCFABEKGKLVAAQAALGL	585
DB	561	QITEQLEAVIADFSGLEKCKCQSQEQVEVCFAEEGQKLISKTRALGV	609

N-LINKED (GLCNAC. . .).
 A->G (IN DBSNP:1057173).
 /FTid-CAR_000070.
 /FTid-VAR_012049.

Search completed: April 24, 2003, 07:22:43
 Job time : 16 secs


```

Db 145 BAMCTSPQENAVTFMGHVLHEVARRHPYFYAPPELLYAEKYSATMTECCGADKAACITP 204
Qy 181 KLDELDRDEGKASSQRLKCLASQKGERAFKAWAVARLSQRFKAEVSKLVTLTK 240
Db 205 KLDALKKALASSYNQRLKCSLQRFQORAFKANAVARMSQKFPKADFAEITKLATDLTK 264
Qy 241 VHTCCCHGDLLECCADRADLAKYICENODSISLKECEKPLLEKSHCHIAEVENDEMPA 300
Db 265 LTECCCHGDLLECCADRAELAKYICENQASISLQACCDKPVLLKSHCLSEVENDDLPA 324
Qy 301 DLPSLAADFVESKDVCKNYAEKAVDFGLMFLYELARRHPDYSVVLLLRKATYETLEK 360
Db 325 DLPSLAADFVEDKEVCNKYAEKAVDFGLTFLYELARRHPDYVALLLRKATYETLEK 384
Qy 361 CAADAPHECAKVEDEKPLVEEPQNLKQCELFQOLGEYKFNALLVRYTKVPQVST 420
Db 385 CAEADPSACYKVLDELQPLVEEPKNLVKANCELFEXLGEYGFONALLVRYTKQAPQVST 444
Qy 421 PTLVEVSRNLGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEAARNLKGKVGSKCKVLPQALPCVEDYISAILNRVCLVHEKTPVSEQVTKCCTGS 504
Qy 481 LVNRRPCFSALEVDVETVYVPKFNATETTFHADICTLSEKEROIKQALVELVYKHKPAT 540
Db 505 VVERPPCSALPVDVETVYVPKFNATETTFHADICTLSEKEROIKQALVELVYKHKPAT 564
Qy 541 KEQLKAVMDDFAAAFVEKCKKADKTCFAEKGKLVAAASQAAL 583
Db 565 GPQLRTVLGERTAFDLKCCRAEDKEACFSEGGPKLVASSQAAL 607

RESULT 2
Q8UW05 PRELIMINARY; PRT; 626 AA.
AC Q8UW05;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Ambystoma maculatum (spotted salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=43114;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and Ambystoma texanum."
RL EMBL: AF217183; AAL56646.1;
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
SQ SEQUENCE 626 AA; 9D66F57F174AC23F CRC64;

Query Match 40.0%; Score 1242; DB 13; Length 626;
Best Local Similarity 40.1%; Pred. No. 1e-86;
Matches 237; Conservative 110; Mismatches 238; Indels 6; Gaps 3;

Qy 1 DANKSEVAHRFKDL-----GGENFKALVLIAPQYLOQCPFEDHVKLVNEYTEFAKTCVAD 56
Db 28 EGHVDNPPLHIGDLIPMIGVDNSKGLVLAASQMLPLCPYEELHQRVEDVQADLCAGK 87
Qy 57 ESEBNCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDN-PNLRL 115

```

```

Db 88 ARHANCAKSPMTIILDELCKKPKNAEKYFPFHQECCKEDPERHKCFVEHKMANHELTKY 147
Qy 116 VRPEVDVMTAFHDEETFLKKYLYETARRHPYVAPPELLFAKRYKAAFTTECCQAADKA 175
Db 148 VRPAEQICDKDAENRGPLLIARYIFMLAIGHPHMYIPAILGFAQRFQDGVSHCKCKDVETA 207
Qy 176 A-CULPLKDELDRDEGKASSQRLKCLASQKGERAFKAWAVARLSQRFKAEVSKLV 234
Db 208 GOCFENDKMPHEKQEVVEVCALQKHCNYLQDFKERALTAYKAVOASQKFPPLASENVQII 267
Qy 235 VTDLTKVHTTECHGDLLECCADRADLAKYICENODSISLKECEKPLLEKSHCHIAEVE 294
Db 268 VPDVTVHLHQTCGGMMACMLERMKLTAKICEKKDELATHLKECCDKPLLSACIIRLP 327
Qy 295 NDEMPADLPSLAADFVESKDVCKNYAEKAVDFGLMFLYELARRHPDYSVVLLLRKATY 354
Db 328 NDQPADLSPKVPHYIDDPEVKLYTEGGDTFMGRFLYECARRHODYSPENLLRMGSGYE 387
Qy 355 TTLEKCAAADPHBCYAKVDFDEKPLVEEPQNLKQCELFQOLGEYKFNALLVRYTKK 414
Db 388 EFLKCCAAEGHNECLAKTESLKEIESSVTLLKTCGALDKLSYLFQNLILFKYVAR 447
Qy 415 VPQVSTPTLVEVSRNLGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRV 474
Db 448 MPALSEQSLRLITKSMTTIGCKCHRPEDQDMTCSEGGIGVFGQICMKQKQKTPVNEKVA 507
Qy 475 KCCTESLVNRRPCFSALEVDVETVYVPKFNATETTFHADICTLSEKEROIKQALVELV 534
Db 508 QCCSHLSISQTPCFESALPVDVETVYPPPLSVASFNFENDELCTTSEPEQSKQVFLIRLMK 567
Qy 535 HKPKATKEQLKAVMDDFAAAFVEKCKKADKTCFAEKGKLVAAASQAALGL 585
Db 568 QYPHMTDEQLKTCVNVFVPMVDQCKKADNINECEFALEGAKLIDACKAILAV 618

RESULT 3
Q8UW06 PRELIMINARY; PRT; 624 AA.
AC Q8UW06;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Ambystoma texanum (Smallmouth salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8304;
RN [1]
RP SEQUENCE FROM N.A.
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and Ambystoma texanum."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF217182; AAL56645.1;
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
SQ SEQUENCE 624 AA; 70321 MW; DE08533BF4953EF7 CRC64;

Query Match 35.0%; Score 1087; DB 13; Length 624;
Best Local Similarity 37.7%; Pred. No. 7.1e-75;
Matches 214; Conservative 102; Mismatches 240; Indels 12; Gaps 5;

Qy 14 LGGENFKALVLIAPQYLOQCPFEDHVKLVNEYTEFAKTCVADSEBNCDSLHTLFGDK 73

```

Db 45 IGVEHAKALAMALFSQMLSKCPHHEQVQRVNVNMDIADLCRGAKHGDCGKSVMTIILNE 104
 QY 74 LCTVATLRETYGEMADCCAKQSPERNECFLOHKDDNP-NLPRLVRPEVDMVCTAFDNEE 132
 Db 105 ICKTPENPKYFPHGECCKKEDPERHKCFIEHKSTDPKERTKTEYKVPSPQICKDHAEND 164
 QY 133 TELKKYLYEIARRHPYFAPPELLFFAKRYKAAFTCCQ-AADKAACLLPKLDELDEGR 191
 Db 165 EFLGHIYHKVASSHTTMYPAIILSFTLHFDGIVSHCCKDEATVGQCLSEKMPAHKEVEH 224
 QY 192 SAKQBLKASLOKQGERAFKAWARLSORPPKAEFAEVSKLVTDLTKVHTECHGDL 251
 Db 225 VCAYOKHNCYIILQNFERNALRASAKAHAGSKFFHASFENVRQRLTDGIVLHOTHCCGDDMM 284
 QY 252 ECADDRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPADLPSLAADFVE 311
 Db 285 ACMAERKLTOTCEK-----KCCCKPVLSECEIVRPNDKPADLSPVEVRYFD 336
 QY 312 SKDVCKNYAEAKDVFGLMFYIYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYA 371
 Db 337 DPEVCKRFEEDGAFMGRFLCDYAKIHPHSAELNRIASGLEKAYKTCCEAGAHNECIA 396
 QY 372 KYFDEKPLVEPONLIKONCELFQOLGEYKFNALLVRYTKYPOVSTPTLVEVSRNLG 431
 Db 397 KEETLRHIEASKTKLTCTGALEKLGYPHFQINIVRYTGILPRSSDAFLYITKILT 456
 QY 432 KYGSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPV-SDRVTKCTTESLVNRRPCFA 490
 Db 457 NGQCKCKLPEDQMPSCSGGLWFAQIC-QNOKTFFENEKLAHCKOSLSFTTTCFRAA 515
 QY 491 LEVDETYVPKEFNAETFFHADICTLSEKERQIKKOTALVELVYKHKPKATKQOLKAVMD 550
 Db 516 LTWDETYVPVPAVTAESFNDEFCTPSEADLOAKQKQTFMLHMLVTRTHPKITDEQVKITSEK 575
 QY 551 FFAFVEKCKADKCTCFABEKGKLVAA 578
 Db 576 FLAMGQCKCKADORNECFATEGAKLVAA 603

RESULT 4

QYGH6 ID QYGH6 PRELIMINARY; PRT; 603 AA.
 AC QYGH6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Serum albumin precursor (Fragment).
 GN ALB.
 OS Rana shqiperica.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=44326;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BUSHAT; TISSUE=LIVER;
 RA Uzzell T., Hotz H.;
 RT "Albumin cDNA sequence of Rana shqiperica: evolutionary changes in
 frog albumins";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40452; AAD09338.1; -;
 DR HSP; P02768; 1E7B.
 DR InterPro; IPR000264; Serum albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Signal.
 FT NON-TER 1 1
 FT SIGNAL <1 23 POTENTIAL.
 FT CHAIN 24 603 SERUM ALBUMIN.
 SQ SEQUENCE 603 AA; 69293 MW; 340D3723FA010C99 CRG64;

Query Match 30.8%; Score 955; DB 13; Length 603;
 Best Local Similarity 33.6%; Pred. No. 8.3e-65;
 Matches 190; Conservative 119; Mismatches 241; Indels 16; Gaps 3;
 QY 12 KDIGENFKALVLIAPQYLOQCPFDHVKLVNEVTEFAKTCVADSAENCDSKSLHTFLG 71
 Db 37 KAVGKPAVEKLVLMVAQDFEKGSLHKLKQAKIIEAVDNCCKHPEAECKKPAIELYH 96
 QY 72 DKLCITVATLRETYGEMADCCAKQEPERNECFLOHKDDNP-LPRLVR-----PEVDVMT 125
 Db 97 DIVCKEEDIDQLYPWTTECGKAEARTKCFYEHRE-----VRVEEYKIPNIEESCK 148
 QY 126 AFHDNETFLKKYIEIARRHPYFAPPELLFFAKRYKAAFTCCQADKAACLLPKLDEL 185
 Db 149 EHKEHPQAFSYLSNIAKHSKLYPPAVLGFAIQYNEITTECCAARDKACGGERMPQV 208
 QY 186 RDEGKASSAKQRLKASLOKQGERAFKAWARLSORPPKAEFAEVSKLVTDLTKVHTEC 245
 Db 209 KKLNTNLEDKHKQKCRVLEKPEPVSQALTLVQVSQFNGAKYDDVEKVTIEIAHLNEDC 268
 QY 246 CHGDLLECADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPADLPSL 305
 Db 269 CKGDVAVECMIERMEATEHICLAKEKLSKUSCCGKGLERTPCILALPNEE--PDLPIE 326
 QY 306 AADFVESKDVCKNYAEAKDVFGLMFYIYARRHPDYSVVLLRLAKTYETTTLEKCCAAAD 365
 Db 327 LXEYDEHVCENYQDKRKYLAHFTHDYSRSHQESSPOSCLRVSRGFMLEKCCASAN 386
 QY 366 PHECYAKVDEDFPLVEEPONLIKONCELFQOLGEYKFNALLVRYTKYKVPQVSTPTLVE 425
 Db 387 SAELCDAPAKLLEALKENEIEISKNGCALEKLGFDNFYIQLLVRYFEGKMPQVTAQTLVE 446
 QY 426 VSRNLKGVSKCKHPEAKRMPCAEDYLSVNLNOLCVLHEKTPVSDRVTKCTTESLVNRR 485
 Db 447 LTRMAKIGVYCCGLPDNKKQPCAEKLDILGEMCERERKTFINDNVHCCVDSYANRR 506
 QY 486 PCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKOTALVELVYKHKPKATKBLK 545
 Db 507 PCFTKLGYPANYEAPVWDESKLHFTADMKCGSADDQLTKLVLLVEFLKMKPTCGKEKLT 566
 QY 546 AVMDFAAFVEKCKCKADKCTCFABE 571
 Db 567 EVIESPRKTVVECCAAENQACFDEK 592
 RESULT 5
 QY1134 ID QY1134 PRELIMINARY; PRT; 614 AA.
 AC QY1134;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Cobra serum albumin.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96145734; PubMed=8561913;
 RA Wang X., Hansen H., Havsteen B.;
 RT "Evidence of the coevolution of snake toxin and its endogenous
 antitoxin. Cloning, sequence and expression of a serum albumin cDNA of
 the Chinese cobra";
 RL Biol. Chem. Hoppe-Seyler 376:545-553(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93343893; PubMed=8343135;
 RA Shao J., Shen H., Havsteen B.;
 RT "Purification, characterization and binding interactions of the


```
QY 4 KSEVAHRFKDLGEENFKALVLIHFAQYLOQCPFEDHVKLVNEVTEFAKTCTVADESAENC 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 RDKVQCEKTKMGKDDFRAMTLTMSKSNFATSEIISHLVHEVMVSLAETCCAGVDPSCY 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 KSLHLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPRLVRYPEVDYM 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 DTGSSALSAKSCSPDPPFPAHPTGAACCLHOGLEKCLLALEHPHPPQLPHYVEPSNEEL 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 CTAFHNEETFLKKYLYETARRHPFYAPPELLFFFAKRYKAATTECCQAADKAACLLPKLD 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 146 CEAFKDKPDAFDRFELHEVSYGGAPLVLGSTRNFLSMVSTCCISPSPTVCFLKEKL 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 ELRDEGKASSAKORLKASLOKGERAFKAWARLSQRFPKAEFAEVSCLKVTDLTVKHT 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 ORKTLISLTLMSNR-ACSLAAYGDKMKFSYLTMLAQIPASPEDLSPLAEDAAEMPS 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 ECHGDLLECCADR-ADLAKYICENQDSISSKLEKCEC-KPLEKSHCIAEVENDEMPAD 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 265 QCCDSVAEDCIQKLESEHTTKCATLSAKDKRFADCCGKNYQNYFCISSLQPAVAP-K 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 LPSLAADFVESDKVCKNTAEAKDVLGMLFLEYARRHPDYSVVLLRLAKTYETTTLEKCC 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 LPELQKP--TNKQLCDNCA---LHTRRYMFEARHRTNVPDYFLGKLYDASENVIKECC 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 AAADPHECY----AKVDEKFLVPEEPQNLIKONCELFQOLGEYKFNAL--LVRYTKV 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 SAKDASSCLDGKRQGMGTPLAFLEKTQDQ----CQYTELNFDFKKRLRDSIRQTR-- 432
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 416 PQVSTPTLVEVSRNLGKVGSKCC 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 PDASPELLTQLDQDRADFASCTCC 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
Q9CY31 PRELIMINARY: PRT; 476 AA.
AC Q9CY31;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Group specific component.
GN GC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaiji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010965; BAB27297.1; -.
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.
```

```
DR Pfam; PF00273; transport_prot; 2.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 2.
DR PROSITE; PS00212; ALBUMIN; 1.
SQ SEQUENCE 476 AA; 53614 MW; 11F2EB7FFA2B0699 CRC64;

Query Match 12.0%; Score 373; DB 11; Length 476;
Best Local Similarity 24.3%; Pred. No. 1.9e-20;
Matches 111; Conservative 76; Mismatches 226; Indels 44; Gaps 11;

QY 1 DAHSEVAHRFKDLGEENFKALVLIHFAQYLOQCPFEDHVKLVNEVTEFAKTCTVADESAE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 DYKCKVVCNELAMLGKEDFRSLILYSRKFSSTEQVNQLVKEVSVLSTECCAGADP 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPNERCEFLQHKDDNPRLVRYPEV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 TCYDTRTSELVSKSCSDAPFPVHPGTPECTKEGLERKLCMAALSHQPOEFPTTVEPTN 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 DVNCTAFHNEETFLKKYLYETARRHPFYAPPELLFFFAKRYKAATTECCQAADKAACLLP 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 DEICEAFRDPKGFADFLYESSNYGQAPLPLLVAYTKNLSWVGSCTTSANPTVCVFK 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 KIDEURDEGKASSAKORLKASLOKGERAFKAWARLSQRFPKAEFAEVSCLKVTDLT 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 ERLQMKHLISLTLTMSNRV-CSQYAAAYGKESKLSHLIKLAQKVPTAKLENVPLAEDFTE 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 VITECHGDLLECC-ADDRADLAKYICENQDSISSKLEKCECPLLEKSHCIAEVENDEM- 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 261 ILSRCCSTSEDCMASLPEHTIKQNLKSNKSEECQ-----ENTPMN 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 -----PADLPSLAADFVESKDYC-KNYAEAKDVLGMLFLEYARRHPDYSVVL 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 IFMCTVFMPEAAEPLQLP--AIKLTGKDLGCGSTTQAMD----QYTFELSRRTQVEVFL 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 LLRLAKTYETTTLEKCCAAADPHECYAKVDFEKPVLVE-EPQNLIKONCELFQOLGEYKFP- 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 SKVLEPTLK-TLRECCDQDSVAC----FSTQSPILKRLQLTSPFERQGMCADYSENTFT 416
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 404 --QNALLVRYTKVPOVSTPTLVEVSRNLGKVGSKCC 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 EYKKLAERLRTKTPNTSPAELKDMVEKHSDFASKCC 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
Q91XG1 PRELIMINARY: PRT; 476 AA.
AC Q91XG1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Group specific component.
GN GC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010762; AAH10762.1; -.
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 2.
DR ProDom; PD002486; Serum_albumin; 1.
DR PROSITE; PS00212; ALBUMIN; UNKNOWN 1.
SQ SEQUENCE 476 AA; 53600 MW; 633B0CE183CD43FD CRC64;

Query Match 12.0%; Score 372; DB 11; Length 476;
Best Local Similarity 24.3%; Pred. No. 2.3e-20;
Matches 111; Conservative 75; Mismatches 227; Indels 44; Gaps 11;
```



```
Db 410 SDLSYLAHDGYRKC-----RLAPSEAVSCHVE-----HERAH 443
Qy 522 QIKKOTALV-----ELVKHKPKATKEQLKAVMDFFAA-----553
: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 EAERATEEVENHGKERVEHQAKV--EAVEAVEAPFAEAGRAARSLRQPLPGKYLQRLLY 501
Qy 554 -----FVE-----KCKKADDKETCFABEGKKL 575
: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 502 KAAHQAPAGVDHSRILQVHFHEVTAKCCRAYDKSCFCSHEIKEM 547

RESULT 11
Q90WZ8 PRELIMINARY; PRT; 122 AA.
AC Q90WZ8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Serum albumin (fragment).
OS Larus argentatus (Herring gull).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Laridae; Larus.
OX NCBI_TaxID=35669;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzen A., Casley W.L., Moon T.W.;
RT "Development of an RT-PCR Bioassay for Avian Vitellogenin mRNA.";
RL Toxicol. Appl. Pharmacol. 0:0-0(2001).
DR EMBL; AY045725; ALA01333.1;
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13805 MW; 93C644A0B120EF93 CRC64;

Query Match 10.7%; Score 331; DB 13; Length 122;
Best Local Similarity 47.1%; Pred. No. 5.9e-18;
Matches 57; Conservative 23; Mismatches 41; Indels 0; Gaps 0;

Qy 452 YLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDITYVPKEFNAETFFHA 511
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : |
Db 1 YLSIVIQMCRQRRTVPVNDVNSHCCSDSYAYRRPCFTAMGVDTKYVPPAFDPFMFSD 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : |

Qy 512 DICTLSEKERQIKKOTALVELVHKPKATKEQLKAVMDFFAAAFVEKCKKADDKETCFABE 571
: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KLCTAPAEQELGQMKLLINLIKRPQMTBEOIKTIADGFTAMVDKCKQSDIETCFGE 120
: : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 572 G 572
|
Db 121 G 121

Query Match 8.5%; Score 264; DB 11; Length 135;
Best Local Similarity 41.0%; Pred. No. 8.9e-13;
Matches 50; Conservative 20; Mismatches 52; Indels 0; Gaps 0;

RESULT 12
Q90WZ6 PRELIMINARY; PRT; 123 AA.
AC Q90WZ6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Serum albumin (fragment).
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
OC Estrilidae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzen A., Casley W.L., Moon T.W.;
RT "Development of an RT-PCR Bioassay for Avian Vitellogenin mRNA.";
RL Toxicol. Appl. Pharmacol. 0:0-0(2001).
DR EMBL; AY045727; ALA01335.1;
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.

FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13824 MW; B18F83BC2E194F29 CRC64;

Query Match 9.3%; Score 290; DB 13; Length 123;
Best Local Similarity 43.0%; Pred. No. 8.2e-15;
Matches 52; Conservative 22; Mismatches 47; Indels 0; Gaps 0;

Qy 452 YLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDITYVPKEFNAETFFHA 511
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : |
Db 1 YLTVIIEDMCKKQESTPVNDQVSCCNDLYSDKRPCFTAMGTDYVVPAPDPTLFDDE 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : |

Qy 512 DICTLSEKERQIKKOTALVELVHKPKATKEQLKAVMDFFAAAFVEKCKKADDKETCFABE 571
: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KMCKAPPAEREAGELKLLVNLVKKRPQMTBEOIKTEGFTAMMEKCKKDPDVEGLCEE 120
: : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 572 G 572
|
Db 121 G 121

RESULT 13
Q63205 PRELIMINARY; PRT; 135 AA.
ID Q63205
AC Q63205;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Messenger RNA for rat alpha-fetoprotein (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81005964; PubMed=6157690;
RA Innis M.A., Miller D.L.;
RT "Alpha-fetoprotein gene expression. Partial DNA sequence and COOH-terminal homology to albumin.";
RL J. Biol. Chem. 255:8994-8996(1980).
DR EMBL; V01236; CAA24546.1;
DR HSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
DR SMART; SM00103; ALBUMIN; 1.
FT NON_TER 1
FT NON_TER 135
SQ SEQUENCE 135 AA; 15040 MW; 0F922DAF4F71EAC4 CRC64;

Query Match 8.5%; Score 264; DB 11; Length 135;
Best Local Similarity 41.0%; Pred. No. 8.9e-13;
Matches 50; Conservative 20; Mismatches 52; Indels 0; Gaps 0;

Qy 450 EDLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDITYVPKEFNAETTF 509
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : |
Db 1 EGLADIVYICHLRHEANPVNSGINSYSSNRRLCTISFLRDETVPPLPFSATNSS 60
: : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 510 HADICTLSEKERQIKKOTALVELVHKPKATKEQLKAVMDFFAAAFVEKCKKADDKETCF 569
: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TRNLCAQAGRAPQTMKQELLINLVKRPQMTBEOIKTEGFTAMMEKCKKDPDVEGLCEE 120
: : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 570 EE 571
|
Db 121 KE 122

RESULT 14
Q9JMX8 PRELIMINARY; PRT; 1723 AA.
ID Q9JMX8
AC Q9JMX8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Cag-y.
```

GN CAG-Y.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG 17874;
RX MEDLINE=97121442; PubMed=8962108;
RA Censini S., Lange C., Xiang Z., Crabtree J.E., Ghiara P.,
Borodovsky M., Rappuoli R., Covacci A.;
RT "cag, a pathogenicity island of Helicobacter pylori, encodes type I-
specific and disease-associated virulence factors";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14648-14653(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG 17874;
RX MEDLINE=20150112; PubMed=10684850;
RA Covacci A., Rappuoli R.;
RT "Tyrosine-phosphorylated bacterial proteins: Trojan horses for the
RT host cell";
RL J. Exp. Med. 191:587-592(2000).
DR EMBL; AF282852; AAF80198.1; -;
SQ SEQUENCE 1723 AA; 196048 MW; 0FAC456B76622801 CRC64;

Query Match 6.1%; Score 188; DB 2; Length 1723;
Best Local Similarity 22.9%; Pred. No. 1.2e-05;
Matches 157; Conservative 88; Mismatches 254; Indels 188; Gaps 37;

QY 16 EENFKALVLIAPAYIQOCPFFEDHVKLVNEVTEFAKTCVADESAENC-----DKSLHTLF 70
DB 351 EERIKLDLIKDNKLLKSLNQKQVQVALDCLKNKNT---DEERNECLKLINDPEIREKF 407
QY 71 GDLKLTATLRETYGEMADCC--AKOEPERNECFLOKDDNPMLPLVRPEVDVMTAFH 128
DB 408 RKEL-----GLQELQYKDCIKNAKTEAEKNECKLSKE--AIERLKQOALDCLKNKNT 461
QY 129 DNEETFLKLYEIAIRRHFFVYAPELL--FFAKRYKAAFTCCQAADKAAC---LLPK 181
DB 462 DEERN-----ECLKNIPQDLQKELLADMSVKAYKDCVSKARNEKEKECEKLLTPEAR 514
QY 182 -----LDELREGKASAKQRLKAS-----LQKFERAFKAWAVARLSQRP 224
DB 515 KLEQOVLQCLKN-----AKTDEERKCKLDPKDLQSDILAKESLKAYKDC---VSQAKT 567
QY 225 KAEFAEVSILVT-----DLTKVHTEC-----CHGDLLECADDRADL 260
DB 568 EAEKKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEKLLTPEAKKLEB 627
QY 261 AK-----YI-CENQDSISSKLEKCE-----KPLLEKS--HCIAEVENDE-----EM 298
DB 628 AKKSVKAYLDCVSOAKTEAEKKECEKLLTPEAKKLLLEQOALDCLKNKNTADKRCVKDL 687
QY 299 PADLPS--LAAD-----FVSKDVCKNYAEAKDVFGLMFLYEVARRHPDYSVVLNLLAKT 352
DB 688 PKDLQKVLAKESVRYLDCVSKARNEKE--CEKLLTPEAK-----LLEAKK 737
QY 353 YETLEKCCAAA-----DPHECYAKVDFEPLVEEPQNLKQNCLEFQEL---GEYKFN 405
DB 738 SVKAYKDCVSRARNEKEKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECE 797
QY 406 ALLVRYTKVPQVSTPTLVE---VSRNLGKGVSKCKH---PEAKRMPCAEADYLSVNLN 458
DB 798 KLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEKLLTPEAKL-----LE 847
QY 459 QL----CVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDYTPKBFNAETFT-----FH 510
DB 848 QOALDCLKNKNTAD---KKRCVKDL-----PKDLQKVLAKESVKAY 887
QY 511 ADICTLSEKQIKK--QTALVELVHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKTC---567
DB 888 LDCVSRARNEKEKECEKLLTPEAKKLLLEBAKESLKAYKD-----CLSQARNEEERACEK 943

QY 568 -----FAEECKKLVA-----SQA 581
DB 944 LLTPEARKLLEAKSKSVKAYLDCVSA 970

RESULT 15
Q9ZLVO PRELIMINARY; PRT; 1819 AA.
ID Q9ZLVO;
AC 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DE 01-MAR-2002 (TREMREL. 20, Last annotation update)
DE CAG island protein.
GN JHP0476.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Gullid B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
DR EMBL; AE001481; AAD06047.1; -;
KW Complete proteome.
SQ SEQUENCE 1819 AA; 207505 MW; E76762B5A7FA371D CRC64;

Query Match 5.9%; Score 184; DB 16; Length 1819;
Best Local Similarity 21.8%; Pred. No. 2.7e-05;
Matches 150; Conservative 101; Mismatches 278; Indels 158; Gaps 34;

QY 16 EENFKALVLIAPAYIQOCPFFEDHVKLVNEVTEFAKTCVADESAENC-----DKSLHTLF 70
DB 371 EERIKLDLIKDNKLLKSLNQKQVQVALDCLKNKNT---DEERNECLKLINDPEIREKF 427
QY 71 GDLKLTATLRETYGEMADCC--AKOEPERNECFLOKDDNPMLPLVRPEVDVMTAFH 128
DB 428 RKEL-----ELQELQYKDCIKNAKTEAEKNECKLSKE--AIERLKQOALDCLKNKNT 481
QY 129 DNEETFLKLYEIAIRRHFFVYAPELL--FFAKRYKAAFTCCQAADKAAC---LLPKLD 183
DB 482 DEERK-----ECLKNIPQDLQKELLADMSVKAYKDCVSRARNEKEKECEKLLTPEAK 534
QY 184 ELRDE-----GKASSAKQRLKAS-----LQKFERAFKAWAVARLSQRPKAE 227
DB 535 KLEQOVLQCLKN-----AKTDEERKCKLDPKDLQSDILAKESLKAYKDC---VSQAKTEAE 590
QY 228 FAEVSKLVT-----DLTKVHTEC-----CHGDLLECADDRADLAK- 262
DB 591 KKECEKLLTPEAKKLLLEBAKESVKAYLDCVSOAKTEAEKKECEKLLTPEAKKLEAK 650
QY 263 -----YI-CENQDSISSKLEKCE-----KPLLEKS--HCIAEVENDE-----MPAD 301
DB 651 SVRAYLDCVSKARNEKEKECEKLLTPEAKKLLLEQOALDCLKNKNTADKRCVKDL 710
QY 302 LPS--LAAD-----FVSKDVCKNYAEAKDVFGLMFLYEVARRHPDYSVVLNLLAKTYET 355
DB 711 LQKVLAKESVRYLDCVSKARNEKE--CEKLLTPEAK-----LLEAKSKVYK 760
QY 356 TLEKCCAAA-----DPHECYAKVDFEPLVEEPQNLKQNCLEFQEL---GEYKFNALL 408
DB 761 AVKDCVLRARNEKEKECEKLLTPEAKKLLLEBAKESVKAYLDCVSKARNEKEKECEKLL 820
QY 409 VRYTKVPQVSTPTL-----VEVSRNLGKGVSKCKH---HPEAKRMPCAEADYLSVNLN 460
DB 821 TPEARKLLEBAKESVKAYKDCVSRARN--EKEQOCEKLLTPEARKL--LEESKSKVAYLD 878

QY 461 CVLHEK-----TPVSDRVTKCTESLVNRRPCFSAL-----EVDETYVPKE 501
Db 879 CVSKAKNEAEKCEKLLTPEARKLLEAKESVKAYKDCVSRARNEKEKECEKLLTPE- 937
QY 502 FNAETFTFHADICTLSEKERQIKKOTALVELYK--HKPKATKEQLKAVMDDFAAFVEKCC 559
Db 938 --AKLLENQALDCLNKAETAEKRRCKVDLPKDLQKKVLAKESVRVYLD----CVSKAK 991
QY 560 KADDKETC---FAEGGKLVAAASQAAL 583
Db 992 NEAEKCEKLLTPEARKLLEAKESV 1018

Search completed: April 24, 2003, 07:24:00
Job time : 44 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2003, 07:22:19 ; Search time 77 seconds
(without alignments)
1012.359 Million cell updates/sec

Title: US-09-833-111-18

Perfect score: 3103

Sequence: 1 DAHSEVAHREKDLGEENFK.....TCFAEGKLVAAQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_101002.*
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	585	10 AAP90388	Mature human serum
2	3103	100.0	585	11 AAR05318	Human serum albumi
3	3103	100.0	585	11 AAR05318	Human serum albumi
4	3103	100.0	585	16 AAR0301	Human serum albumi
5	3103	100.0	585	18 AAO20111	HSA protein sequen
6	3103	100.0	585	21 AAY84873	Amino acid sequenc
7	3103	100.0	585	21 AAY83946	Yeast codon-biased
8	3103	100.0	585	22 ABB79006	Human mature album
9	3103	100.0	585	22 AAE13399	Human albumin (HA)
10	3103	100.0	585	22 AAM52567	Mature human serum

11	3103	100.0	585	22 AAE13129	Human albumin (HA)
12	3103	100.0	585	22 AAE12403	Human albumin (HA)
13	3103	100.0	585	22 AAE08578	Human serum albumi
14	3103	100.0	585	23 ABG63321	Human serum albumi
15	3103	100.0	585	23 ABJ00986	B lymphocyte stimu
16	3103	100.0	585	23 ABG33847	Human B lymphocyte
17	3103	100.0	585	23 AAU75220	Mature form of hum
18	3103	100.0	609	21 AAB36542	Recombinant human
19	3103	100.0	609	21 AAB36549	Recombinant human
20	3103	100.0	609	21 AAY78147	Pre human serum al
21	3103	100.0	610	14 AAR39510	Chimeric human ser
22	3103	100.0	670	21 AAB36543	Recombinant human
23	3103	100.0	670	21 AAB36550	Recombinant human
24	3103	100.0	783	14 AAR39473	Prepro-HSA-G-CSF c
25	3103	100.0	787	14 AAR39477	G-CSF-(Gly)4-HSA c
26	3103	100.0	853	14 AAR39472	Sequence of mature
27	3099	99.9	585	10 AAP93344	Sequence of mature
28	3099	99.9	585	19 AAW59841	Mature protein of
29	3099	99.9	608	17 AAR96229	Human serum albumi
30	3099	99.9	609	4 AAP30089	Sequence of human
31	3099	99.9	609	17 AAR96232	Human serum albumi
32	3099	99.9	609	17 AAR94572	Cancer metastasis
33	3099	99.9	609	17 AAR88913	Human serum albumi
34	3099	99.9	609	19 AAW48095	Human serum albumi
35	3099	99.9	609	20 AAY06994	Human albumin. Ho
36	3099	99.9	609	22 AAB04148	Myosin light chain
37	3097	99.8	779	18 AAW22719	Human serum albumi
38	3097	99.8	784	18 AAW22717	Human serum albumi
39	3097	99.8	784	18 AAW22718	Human serum albumi
40	3097	99.8	794	18 AAW22720	Human serum albumi
41	3096	99.8	609	7 AAP60092	Sequence of prepro
42	3095	99.7	586	8 AAP70767	Human serum albumi
43	3095	99.7	609	13 AAR25309	HSA. Pichia pasto
44	3095	99.7	754	17 AAR92149	HSA:Fc gamma RII f
45	3095	99.7	978	19 AAW48096	Human serum albumi

ALIGNMENTS

RESULT 1
AAP90388
ID AAP90388 standard; protein; 585 AA.
AC AAP90388;
XX
DT 01-NOV-1989 (first entry)
XX
DE Mature human serum albumin polypeptide.
XX
KW Human serum albumin; mature protein; new polypeptides;
KW plasma expanders.
XX
OS Homo sapiens (Human).
PN EP322094-A.
PD 28-JUN-1989.
XX
XX 25-OCT-1988; 88EP-0310000.
XX
PR 30-OCT-1987; 87GB-0025529.
XX
XX (DELTA) DELTA BIOTECH LTD.
XX
PI Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX
DR WPI; 1989-186464/26.
XX
DR N-PSDB; AAN90128.
XX
PT New N-terminal fragments of human serum albumin
PT - esp. useful as blood plasma expanders.
XX

PS Disclosure; fig 2; 20pp; English.

XX Mature protein of human serum albumin (see corresp. AAN90128).
CC Used to make new N-terminal fragments which are used as plasma
CC expanders, or as substitutes for HSA or BSA, in tissue culture
CC media.
XX
XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DAHSEVAHFRKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
QY 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
DB 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360
QY 361 CAAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
DB 361 CAAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
DB 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480
QY 481 LVNRRPCFSALEVDETYVPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 481 LVNRRPCFSALEVDETYVPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
QY 541 KEOLKAVMDDFAAFVEKCKCKADDDKCTCFABEGKKLVAASQAALGL 585
DB 541 KEOLKAVMDDFAAFVEKCKCKADDDKCTCFABEGKKLVAASQAALGL 585

RESULT 2
AAR05318

ID AAR05318 standard; protein; 585 AA.

XX AAR05318;

AC AAR05318;

DT 08-OCT-1990 (first entry)

XX Human serum albumin gene product.

XX Human serum albumin; HSA-A; yeast; ds.

XX Homo sapiens.

OS JP02117384-A.

XX 01-MAY-1990.

XX 26-OCT-1988; 88JP-0268302.

XX

PR 26-OCT-1988; 88JP-0268302.

XX (TOFU) TOA NENRYO KOGYO KK.

PA WPI; 1990-176228/23.

XX N-PSDB; AAQ04719.

DR Human serum albumin prepn. by yeast host -

XX by culturing transformed plasmid yeast to produce serum, and

PT removing it.

XX Disclosure; : pp; Japanese.

XX Mature HSA-A may be produced using the sequence incorporated into a

CC plasmid vector with suitable controllers, and transferred to a yeast

CC expression system.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 11; Length 585;

Best Local Similarity 100.0%; Pred. No. 1e-254;

Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60

DB 1 DAHSEVAHFRKDLGGENFKALVLI AFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120

DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120

QY 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

DB 121 DVNCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

QY 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240

DB 181 KLDELDEGKASSAKORLKCASLQKGERAFKAWAVARLSORPPKAEFAEVSCLVTDLT 240

QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300

DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVENDEMPA 300

QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360

DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTLEK 360

QY 361 CAAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420

DB 361 CAAADPHECYAKVDFEFPKLVPEEPQNLKQNCLEFQGLGEYKFQNALLVRYTKKVPQVST 420

QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480

DB 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTES 480

QY 481 LVNRRPCFSALEVDETYVPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540

DB 481 LVNRRPCFSALEVDETYVPKFEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540

QY 541 KEOLKAVMDDFAAFVEKCKCKADDDKCTCFABEGKKLVAASQAALGL 585

DB 541 KEOLKAVMDDFAAFVEKCKCKADDDKCTCFABEGKKLVAASQAALGL 585

RESULT 3

AAR08457

ID AAR08457 standard; Protein; 585 AA.

XX AAR08457;

AC AAR08457;

XX 16-APR-1991 (first entry)

DT 16-APR-1991 (first entry)

XX

DE Human serum albumin.
 XX HSA; folding; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 123..303.
 FT /label= A
 FT Region 1..303
 FT /label= B
 FT Region 123..585
 FT /label= C
 XX
 PN JP0227079-A.
 XX
 PD 25-AUG-1989.
 XX
 PF 10-SEP-1990; 90JP-0250926.
 XX
 PR 06-OCT-1988; 88JP-0250926.
 XX
 PA (TOFU) TONEN CORP.
 XX
 XX WPI; 1990-317325/42.
 DR N-PSDB; AAQ06099.
 XX
 PT New human serum albumin fragments - used to bond medicines and for
 PT stable folding of protein(s).
 XX
 PS Claim 1; Fig 8; 24pp; Japanese.
 XX
 CC Fragments A-C of HSA are expressed as fusion proteins with the
 CC signal peptide of E. coli alkaline phosphatase. The fragments are
 CC selected for their specific properties. The C-terminal truncated
 CC fragment, B, does not bind long-chain fatty acids but does bind to
 CC various medicines at the central region. The N-terminal truncated
 CC fragment, C, has good stability in protein folding. The central
 CC segment, A, has characteristics of both B and C.
 CC See also AAQ06099-Q06098.
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPEFDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPEFDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 QY 121 DVMTAFHNDNETFLKKYLYETARHPYFYAPPELLFFAKRYKAAFTCCQADRAACLLP 180
 DB 121 DVMTAFHNDNETFLKKYLYETARHPYFYAPPELLFFAKRYKAAFTCCQADRAACLLP 180
 QY 181 KIDELRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEYVSKLVTDLTK 240
 DB 181 KIDELRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEYVSKLVTDLTK 240
 QY 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLEKCECKPLLEKSHCIAEVENDEMPA 300
 DB 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLEKCECKPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVSKOVCKNYAEAKOVFLGMFLYFYARRHPDYSVVLLLLAKTYETTLK 360
 DB 301 DLPSLAADFVSKOVCKNYAEAKOVFLGMFLYFYARRHPDYSVVLLLLAKTYETTLK 360
 QY 361 CAADPHCEYAKVDFEFKPLVEEPONLIKQNCLEFQELGVEYKFNALLVRYTKKVPQYST 420
 DB 361 CAADPHCEYAKVDFEFKPLVEEPONLIKQNCLEFQELGVEYKFNALLVRYTKKVPQYST 420

DB 361 CAADPHCEYAKVDFEFKPLVEEPONLIKQNCLEFQELGVEYKFNALLVRYTKKVPQYST 420
 QY 421 PTLVEVSRLKVGSKCKCKHPEAKRMPCAEDYLSVVLNQLCVLHKEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRLKVGSKCKCKHPEAKRMPCAEDYLSVVLNQLCVLHKEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSKERQIKKOTALVELVKKHKPAT 540
 DB 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSKERQIKKOTALVELVKKHKPAT 540
 QY 541 KEQLKAVMDFAAFVEKCKKADDKETCFAEEGKKLVAASQAALGL 585
 DB 541 KEQLKAVMDFAAFVEKCKKADDKETCFAEEGKKLVAASQAALGL 585
 RESULT 4
 AAR80301
 ID AAR80301 standard; Protein; 585 AA.
 AC AAR80301;
 XX 17-JAN-1996 (first entry)
 DT Human serum albumin.
 DE
 XX Serum albumin; HSA; aspartyl protease-3; Yap3p;
 KW Saccharomyces cerevisiae.
 XX Homo sapiens.
 OS
 XX WO9523857-A1.
 PN
 XX 08-SEP-1995.
 PD
 XX 01-MAR-1995; 95WO-GB00434.
 PF
 XX 05-MAR-1994; 94GB-0004270.
 PR
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA
 XX Gilbert SC, Kerry-Williams SM;
 PT
 XX WPI; 1995-320572/41.
 DR N-PSDB; AAQ98695.
 DR
 XX Yeast with reduced levels of aspartyl protease 3 proteolytic
 PT activity - used to secrete human albumin without prodn. of the 45
 PT kD fragment
 XX
 PS Example 1; Page 26-28; 50pp; English.
 XX
 CC The cDNA given in AAQ98695, which encodes HSA (AAR80301), was subjected
 CC to site-directed mutagenesis to investigate the role of
 CC endoproteases in the generation of a 45 kDa albumin fragment obtd.
 CC when the cDNA is expressed in S. cerevisiae. Mutations were: R410A;
 CC L407A, L408V, V409A; and R410A, K413Q, K414Q. The latter set of
 CC mutations, especially, improved stability of HSA to yeast Yap3p
 CC proteolytic cleavage, allowing increased prodn. of recombinant HSA.
 XX
 SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 16; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPEFDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHRFKDLGEENFKALVLIAPFAQYLQOCPEFDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120

121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEYENDEMPA 300
241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEYENDEMPA 300
301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYIYARRHPDYSVLLIRLAKTYETTLEK 360
301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYIYARRHPDYSVLLIRLAKTYETTLEK 360
361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQLGGEYKFNALLVRYTKKVPQVST 420
361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQLGGEYKFNALLVRYTKKVPQVST 420
421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTALVELVKKHPKAT 540
481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTALVELVKKHPKAT 540
541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585

W097 12-44-15

RESULT 5
AAO20111
ID AAO20111 standard; Protein: 585 AA.
XX AAO20111;
XX AC
XX DT
XX 06-AUG-2002 (first entry)
XX HSA protein sequence related to the growth hormone protein.
XX Serum albumin-growth hormone fusion protein; growth hormone;
XX Down's syndrome.
XX Unidentified.
XX KR99076789-A.
XX 15-OCT-1999.
XX 25-JUN-1998; 98RR-0704914.
XX 30-DEC-1995; 95GB-0026733.
XX 19-DEC-1996; 96WO-GB03164.
XX (DELTA) DELTA BIOTECHNOLOGY LTD.
XX WPI; 1997-363680/55.
XX N-PSDB; AAK99568.
XX Serum albumin-growth hormone fusion protein - useful to treat growth
XX hormone related diseases, e.g. Down's syndrome
XX Disclosure; Fig 6; 21pp; Korean.
XX The invention relates to a serum albumin-growth hormone fusion protein -
XX useful to treat growth hormone related diseases such as Down's syndrome.
XX This sequence represents a HSA protein related to the serum albumin-
XX growth hormone protein of the invention.
XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 18; Length 585;
Best Local Similarity 100.0%; Pred No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFDLGBENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKSEVAHRFDLGBENFKALVLIAPQYLOQCPEFDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDPNLRLVRPEV 120
QY 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
DB 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLTk 240
QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEYENDEMPA 300
DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEYENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYIYARRHPDYSVLLIRLAKTYETTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLYIYARRHPDYSVLLIRLAKTYETTLEK 360
QY 361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQLGGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQLGGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
DB 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKKCTES 480
QY 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTALVELVKKHPKAT 540
DB 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTALVELVKKHPKAT 540
QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
RESULT 6
AAO20111
ID AAO20111 standard; protein: 585 AA.
XX AAO20111;
XX AC
XX DT
XX 08-AUG-2000 (first entry)
XX Amino acid sequence of a human albumin protein.
XX Human; albumin; ischemic state; serum protein; metal ion salt;
XX peroperative ischemia; ischemia; myocardial infarction;
XX progressive coronary artery disease.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "optionally acetylated, and claimed under
XX claim 56"
XX WO200020840-A1.
XX 13-APR-2000.
XX 01-OCT-1999; 99WO-US22905.
XX

PR 02-OCT-1998; 98US-0102738.
 PR 02-OCT-1998; 98US-0165581.
 PR 02-OCT-1998; 98US-0165926.
 PR 11-JAN-1999; 99US-0115392.
 XX (ISCH-) ISCHEMIA TECHNOLOGIES INC.
 PA Bar-Or D, Lau E, Winkler JV;
 XX WPI; 2000-303843/26.

XX New method for the continuous detection of ischemic states comprises
 PT detecting and quantifying the existence of an alteration of the serum
 PT protein albumin -

PS Disclosure; Page 97-100; 105pp; English.

XX The present sequence represents human albumin protein. The specification
 CC describes a method for the continuous detection of ischemic states. The
 CC method comprises detecting and quantifying the existence of an alteration
 CC of the serum protein albumin. The method comprises contacting a
 CC biological sample containing albumin from the patient with an excess
 CC quantity of a metal ion salt, where the metal ion binds to the N-terminus
 CC of naturally occurring human albumin, to form a mixture containing bound
 CC metal ions and unbound metal ions, and then determining the amount of
 CC metal ions bound to the albumin N-terminus. The amount of bound metal
 CC ions is correlated to a known value to determine the occurrence or
 CC non-occurrence of an ischemic event. The methods are useful for detection
 CC of ischemic states. The methods are also useful for distinguishing
 CC peroperative ischemia from ischemia caused by , amongst other things,
 CC myocardial infarctions and progressive coronary artery disease.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 Qy 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
 Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARLSORFPKAEVSKLVTDLTK 240
 Db 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARLSORFPKAEVSKLVTDLTK 240
 Qy 241 VHTTECHGDLLECADRADLAKYICENQDSISSKKECCERPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKKECCERPLLEKSHCIAEVENDEMPA 300
 Qy 301 DLPSLAADFVESKDVCKNYAKADKDFLGMFLYFYARRHPDYSVLLLRKATYETTLK 360
 Db 301 DLPSLAADFVESKDVCKNYAKADKDFLGMFLYFYARRHPDYSVLLLRKATYETTLK 360
 Qy 361 CAADDPHCYAKVDFEPLVEEQNLKQNCFLFEQGLGEYKFNALLVRYTKVPQVST 420
 Db 361 CAADDPHCYAKVDFEPLVEEQNLKQNCFLFEQGLGEYKFNALLVRYTKVPQVST 420
 Qy 421 PTLVEVSRNLKGVSKCKHPKARMPCAEDYLSVNLQNLVLEHKTVPVSRVTKCCTES 480
 Db 421 PTLVEVSRNLKGVSKCKHPKARMPCAEDYLSVNLQNLVLEHKTVPVSRVTKCCTES 480
 Qy 481 LVNRRPCFSALEVDYETVYPKEFNAETFTFHADICTLSEKQIKKQATLVELVHKPKAT 540
 Db 481 LVNRRPCFSALEVDYETVYPKEFNAETFTFHADICTLSEKQIKKQATLVELVHKPKAT 540

Qy 541 KEQLKAVMDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585
 Db 541 KEQLKAVMDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585

RESULT 7

AY83946
 ID AY83946 standard; Protein; 585 AA.

AC AY83946;

DT 28-JUL-2000 (first entry)

DE Yeast codon-biased recombinant human serum albumin protein.

XX Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
 KW overlapping oligonucleotide; expression vector.

XX Homo sapiens.

OS Synthetic.

PN CN1239103-A.

PD 22-DEC-1999.

PF 17-JUN-1998; 98CN-0102506.

PR 17-JUN-1998; 98CN-0102506.

PA (HAIJ-) HAIJI BIOENGINEERING CO LTD.

PI Li S, Lu D;

DR WPI; 2000-351198/31.

DR N-PSDB; AAA10091.

PT Process for preparing recombinant human serum albumin - which comprises
 PT yeast biased sex codons

PS Disclosure; Fig 1; 44pp; Chinese.

XX The method relates to a method of recombinantly producing human serum
 CC albumin (HSA) in yeast by altering the coding sequence of HSA to
 CC comprise a yeast codon bias. The complete HSA gene (AAA10091) was
 CC generated as three synthetic fragments (AAA10092-10094) joined by
 CC recombinant DNA technology. Each HSA fragment was synthesized from
 CC overlapping oligonucleotide fragments that were extended. This sequence
 CC represents the complete sequence of the HSA encoded by the human gene
 CC with a yeast codon bias. The invention also covers a recombinant
 CC expression vector, yeast host cells carrying the recombinant expression
 CC vector and the process for producing human serum albumin in the yeast
 CC host cell, especially in secretory mode.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIATAFYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
 Qy 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAFTCCQAADKAACLLP 180
 Qy 181 KLDELDRDEGKASSAKQRLKASLOKFGRAFKAFAVARLSORFPKAEVSKLVTDLTK 240

Db 181 KLDLDRGRASSAKQRLKCSLQKFCERAFKAWAVARLQREPKAEVSKLVTDLT 240
QY 241 VHTPECCGDLLECCADDRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 300
Db 241 VHTPECCGDLLECCADDRADLAKYICENQDSISSKLECCCKPILLESKSHCIAEVENDEMPA 300
QY 301 DLPSLAADRVESKDVCKNYAEAKDVFLGMPFLYEYARRHPDYSVVLLRLAKTYETTTLEKC 360
Db 301 DLPSLAADRVESKDVCKNYAEAKDVFLGMPFLYEYARRHPDYSVVLLRLAKTYETTTLEKC 360
QY 361 CAADPHCEYAKVDFEKPILVEEPQNLKQNCSELFQGEYKFNQALLVRYTKKVPQVST 420
Db 361 CAADPHCEYAKVDFEKPILVEEPQNLKQNCSELFQGEYKFNQALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGKVGSKCKKHPKRAKMPCAEDYLSVVLNQLCVLHKEKTPVSDRYTKCCTES 480
Db 421 PTLVEVSRLNGKVGSKCKKHPKRAKMPCAEDYLSVVLNQLCVLHKEKTPVSDRYTKCCTES 480
QY 481 LVNRRPCFSALEVDYTVPKFEFNAETFTFHADICTLSEKERQIKKOTATVLYLVKHKPKAT 540
Db 481 LVNRRPCFSALEVDYTVPKFEFNAETFTFHADICTLSEKERQIKKOTATVLYLVKHKPKAT 540
QY 541 KEOLKAVMDFFAAFEVKCKKADKDKTCFABEGKKLVAASQAALGL 585
Db 541 KEOLKAVMDFFAAFEVKCKKADKDKTCFABEGKKLVAASQAALGL 585

RESULT 8

ABB79006
ID ABB79006 standard; Protein: 585 AA.

XX ABB79006;

AC 01-AUG-2002 (first entry)

DT Human mature albumin protein SEQ ID NO:18.

DE Human; growth hormone; hGH; albumin; human serum albumin; HSA;
KW albumin fusion protein; cytostatic; anorectic; immunosuppressive;
KW antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer;
KW non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis;
KW type I diabetes mellitus; rheumatoid arthritis.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Domain 1..194
FT /label= 1
FT Domain 1..105
FT /label= subdomain
FT Disulfide-bond 53..62
FT Disulfide-bond 75..91
FT Disulfide-bond 90..101
FT Region 106..119
FT /note= "flexible inter-subdomain linker region"
FT Domain 120..194
FT /label= subdomain
FT Disulfide-bond 124..169
FT Disulfide-bond 168..177
FT Domain 195..387
FT /label= 2
FT Domain 195..291
FT /label= subdomain
FT Disulfide-bond 245..253
FT Disulfide-bond 285..279
FT Disulfide-bond 278..289
FT Region 292..315
FT /note= "flexible inter-subdomain linker region"
FT Domain 316..387
FT /label= subdomain
FT Disulfide-bond 316..361
FT Disulfide-bond 360..369

FT Domain 388..585
FT /label= 3
FT Domain 388..491
FT /label= subdomain
FT Disulfide-bond 392..438
FT Disulfide-bond 437..448
FT Disulfide-bond 461..477
FT Disulfide-bond 476..487
FT Region 492..511
FT /note= "flexible inter-subdomain linker region"
FT Domain 512..585
FT Disulfide-bond 514..559
FT Disulfide-bond 558..567

XX WO200179442-A2.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US11850.

XX 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseltine WA;
PI WPI; 2001-611723/70.

XX N-PSDB; ABN87288.

XX New albumin fusion proteins, useful for treating diseases and disorders
such as cancer, comprise therapeutic protein fused to albumin -
Claim 1; Fig 11; 413pp; English.

XX The present invention describes an albumin fusion protein (I) comprising
a therapeutic protein: X and (a*fragment or variant of) albumin
comprising a the fully defined sequence in ABB79006 of 585 amino acids,
(where the fragment or variant has albumin or therapeutic protein: X
activity). (I) can have cytostatic, anorectic, immunosuppressive,
antidiabetic, antirheumatic, antiarthritic and psoriatic activities.
CC Albumin fusion proteins are stabilised therapeutic proteins e.g.
CC antibodies to C5, C242 and CD80 useful for treating various diseases
and disorders such as non-Hodgkin's lymphoma, cancer, obesity,
transplant rejection, type I diabetes mellitus, rheumatoid arthritis
and psoriasis. Fusing albumin to therapeutic proteins stabilises the
therapeutic protein, extends the shelf life and retains the in vitro or
in vivo biological activity. It also reduces the need to formulate
protein solutions with large excesses of carrier proteins to prevent
loss of therapeutic proteins due to factors such as binding to the
container. The fusion proteins are easily dispensed with a simple
formulation requiring minimal post storage manipulation. The fusion of
therapeutic proteins to albumin confers stability in aqueous or other
solution. The present sequence represents the mature human albumin (HA)
protein which is used in the exemplification of the present invention.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFDLGEENFKALVLIATFAQYLOCCPEDHVKLVNTEFAKTCVADESAE 60
DB 1 DAHKSEVAHRFDLGEENFKALVLIATFAQYLOCCPEDHVKLVNTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
QY 121 DVNCTAFHDNEETFLKKLYEIAARRHPYFAPPELLFFAKRYKAAFTFCCQAADKAACLLP 180

Appendix

Db 121 DVNCTAFHDNEETFLKYLIEIARRHPYFAPPELLFFAKRYKAAFTCCQAAADKACLLP 180
Qy 181 KLDELDRSGKASSAKORLKCSAQKGFGRFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Db 181 KLDELDRSGKASSAKORLKCSAQKGFGRFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Qy 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVSKDVCKNYAKADVFLGMFLYEAARRHPDYSVLLLRLLAKTYETTLK 360
Db 301 DLPSLAADFVSKDVCKNYAKADVFLGMFLYEAARRHPDYSVLLLRLLAKTYETTLK 360
Qy 361 CAADPHCEYAKVDFEFPKLYEPEONLIKONCELFQELGEYKFNALLVRYTKKVPQYST 420
Db 361 CAADPHCEYAKVDFEFPKLYEPEONLIKONCELFQELGEYKFNALLVRYTKKVPQYST 420
Qy 421 PTLVEVSRNLGKVGSKCKHPKAKMPCAEYLSVNLQCLVLEHETKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPKAKMPCAEYLSVNLQCLVLEHETKTPVSDRVTKCCTES 480
Qy 481 LVNRRPCFSALEVDYTPVPEKFNATFTFHADICTLSEKERQIKKQATLVELVHKHPRAT 540
Db 481 LVNRRPCFSALEVDYTPVPEKFNATFTFHADICTLSEKERQIKKQATLVELVHKHPRAT 540
Qy 541 KEQLKAVMDFAAFVEKCKKADKTCFAEAGKKLVAAASQAALGL 585
Db 541 KEQLKAVMDFAAFVEKCKKADKTCFAEAGKKLVAAASQAALGL 585

RESULT 9
AAEL1399
ID AAEL1399 standard; Protein: 585 AA.
XX
AC AAEL1399;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human albumin (HA) protein.
XX
KW Human; albumin; HA; fusion protein; immune system disorder; syphilis;
KW transplant rejection; blood related disorder; myocardial infarction;
KW hyperproliferative disorder; acute myeloid leukaemia; renal disorder;
KW glomerulonephritis; cardiovascular disorder; arrhythmia; rhinitis;
KW respiratory disorder; neurological disease; Alzheimer's disease;
KW endocrine disorder; pheochromocytoma; reproductive system disorder;
KW measles; gastrointestinal disorder; irritable bowel syndrome; HIV;
KW human immunodeficiency virus; wound healing; renal cell carcinoma;
KW melanoma; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 54..61
FT /label= Loop_I
FT 76..89
FT /label= Loop_II
FT 92..100
FT /label= Loop_III
FT 170..176
FT /label= Loop_IV
FT 247..252
FT /label= Loop_V
FT 266..277
FT /label= Loop_VI
FT 280..288
FT /label= Loop_VII
FT 362..368
FT /label= Loop_VIII
FT 439..447
FT /label= Loop_IX

FT Domain 461..475
FT /label= Loop_x
FT Domain 478..486
FT /label= Loop_XI
FT Domain 560..566
FT /label= Loop_XII
XX WO200179258-A1.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US12008.
XX 12-APR-2000; 2000US-229358P.
PR 25-APR-2000; 2000US-199384P.
PR 21-DEC-2000; 2000US-256931P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX Rosen CA, Sadeghi H, Prior CP, Turner AJ;
XX WPI; 2001-602931/68.
DR N-PSDB; AAD22287.
XX Albumin fusion proteins comprising a therapeutic protein and albumin,
XX useful in the treating metastatic renal cell carcinoma, metastatic
XX melanoma, malignant melanoma, renal cell carcinoma, HIV (human
XX immunodeficiency virus) or infection -
PS Claim 1; Fig 9; 325pp; English.
XX
CC The invention relates to albumin fusion proteins comprising therapeutic
CC protein and human albumin (HA). The albumin fusion proteins are useful
CC in the treatment, prevention, diagnosis, and/or detection of diseases,
CC disorders such as immune system disorders (transplant rejection); blood
CC related disorders (myocardial infarction); hyperproliferative disorders
CC (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis);
CC cardiovascular disorders (arrhythmias); respiratory disorders
CC (non-allergic rhinitis); neurological diseases (Alzheimer's disease);
CC endocrine disorders (pheochromocytoma); reproductive system disorders
CC (syphilis); infectious diseases (measles); gastrointestinal disorders
CC (irritable bowel syndrome) and wound healing. The albumin fusion
CC proteins are also used in the treatment of metastatic renal cell
CC carcinoma, metastatic melanoma, malignant melanoma and HIV (human
CC immunodeficiency virus) infection. Nucleic acid encoding albumin fusion
CC protein is useful in gene therapy. The present sequence is human
XX albumin (HA) protein.
SQ Sequence 585 AA;
Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFKDLGGEENFKALVLAFAQYLOQCFEDHVKLVNEVTEFAKTCVADESAE 60
Db 1 DAHKSEVAHRFKDLGGEENFKALVLAFAQYLOQCFEDHVKLVNEVTEFAKTCVADESAE 60
Qy 61 NCDSLSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 61 NCDSLSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Qy 121 DVNCTAFHDNEETFLKYLIEIARRHPYFAPPELLFFAKRYKAAFTCCQAAADKACLLP 180
Db 121 DVNCTAFHDNEETFLKYLIEIARRHPYFAPPELLFFAKRYKAAFTCCQAAADKACLLP 180
Qy 181 KLDELDRSGKASSAKORLKCSAQKGFGRFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Db 181 KLDELDRSGKASSAKORLKCSAQKGFGRFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Qy 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCECHGDLLECADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300

Handwritten signature

Db 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
AAW52567
ID AAW52567 standard; Protein: 585 AA.
XX
AC AAW52567;
XX
DT 05-FEB-2002 (first entry)
DE Mature human serum albumin.
XX
KW Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiant;
KW nootropic; neuroprotective; gene therapy; immune disorder; wound healing;
KW hyperproliferative disorder; renal disorder; cardiovascular disorder;
KW respiratory disorder; neurological disease; endocrine disorder;
KW reproductive system disorder; infectious disease;
XX
XX gastrointestinal disorder.
XX
OS Homo sapiens.
XX
XX WO200179444-A2.
XX
XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US12013.
XX
XX 12-APR-2000; 2000US-229358P.
XX 25-APR-2000; 2000US-199384P.
XX 21-DEC-2000; 2000US-256931P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haseltine WA;
XX
XX WPI: 2001-616755/71.
XX N-PSDB; ABA03057.
XX
XX Albumin fusion proteins comprising a therapeutic protein and albumin,
XX useful in the treating immune system disorders (e.g. transplant
XX rejection), blood related disorders (e.g. myocardial infarction) and
XX hyperproliferative disorders -
XX
XX Claim 1; Fig 15; 606pp; English.
XX
XX The present invention relates to albumin fusion proteins, which comprise
XX a therapeutic protein and albumin. The present sequence is the protein
XX sequence for mature human serum albumin (HA), which was used to generate
XX the fusion proteins of the present invention. The albumin fusion proteins
XX are useful in the treatment, prevention, diagnosis, and/or detection of
XX diseases/disorders such as immune system disorders (e.g. transplant
XX rejection), blood related disorders (e.g. myocardial infarction),

CC hyperproliferative disorders (e.g. childhood acute myeloid leukemia),
CC renal disorders (e.g. glomerulonephritis), cardiovascular rhinitis (e.g.
CC arrhythmias), respiratory disorders (e.g. non-allergic rhinitis),
CC neurological diseases (e.g. Alzheimer's disease), endocrine disorders
CC (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis),
CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
CC irritable bowel syndrome) and wound healing.
XX
SQ Sequence 585 AA;
Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHSEVAHFRKDLGDFKALVIAFAQYLOQCPEFHDHVKLVNEVTEFAKTCVADSAE 60
DB 1 DAHSEVAHFRKDLGDFKALVIAFAQYLOQCPEFHDHVKLVNEVTEFAKTCVADSAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVPEV 120
QY 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKYLIEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKORLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
DB 181 KLDELDEGKASSAKORLKCSLQKGERAFKAWAVARLSQRPKAEFAEVSCLVTDLT 240
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHPDYSVVLLRLAKTYETTLEK 360
QY 361 CAADPHCEYAKVDFEKPVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKPVOST 420
DB 361 CAADPHCEYAKVDFEKPVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKPVOST 420
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVNLQNLVLEHKTPTVSDRVTCKCTES 480
DB 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVNLQNLVLEHKTPTVSDRVTCKCTES 480
QY 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHPKAT 540
QY 541 KEQLKAVMDDFAAVFEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585
DB 541 KEQLKAVMDDFAAVFEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585
RESULT 11
AAE13129
ID AAE13129 standard; Protein: 585 AA.
XX
AC AAE13129;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human albumin (HA).
XX
XX Human; albumin; HA; fusion protein; therapeutic protein; vulnary;
XX immune system disorder; transplant rejection; blood related disorder;
KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;
KW childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia;
KW respiratory disorder; gene therapy; non-allergic rhinitis; nootropic;
KW neurological disease; Alzheimer's disease; reproductive system disorder;
KW endocrine disorder; pheochromocytoma; infectious disease; antiarthritic;
KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;

wound healing; antiinflammatory; immunosuppressive; neuroprotective; cardiant; cytostatic; antileukaemic; antirheumatic; antimicrobial; renal disorder.
Homo sapiens.

Key Location/Qualifiers
Domain 54..61 /label= Loop_I
Domain 76..89 /label= Loop_II
Domain 92..100 /label= Loop_III
Domain 170..176 /label= Loop_IV
Domain 247..252 /label= Loop_V
Domain 266..277 /label= Loop_VI
Domain 280..288 /label= Loop_VII
Domain 362..368 /label= Loop_VIII
Domain 439..447 /label= Loop_IX
Domain 461..475 /label= Loop_X
Domain 478..486 /label= Loop_XI
Domain 560..566 /label= Loop_XII

WO200179443-A2.

25-OCT-2001.

12-APR-2001; 2001WO-US11924.

12-APR-2000; 2000US-229358P.

25-APR-2000; 2000US-199384P.

21-DEC-2000; 2000US-256931P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

WPI; 2001-616754/71.

N-PSDB; AAD21638.

Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -

Claim 1; Fig 9; 380pp; English.

The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). Therapeutic protein fused to albumin have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is human albumin (HA) protein.

Sequence 585 AA;

Query Match		100.0%;	Score 3103;	DB 22;	Length 585;
Best Local Similarity		100.0%;	Pred. No. 1e-254;		
Matches 585;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DAHKSEVAHRFKDGLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60	
DB	1	DAHKSEVAHRFKDGLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60	
QY	61	NCOKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPMLPLVRPEV	120		
DB	61	NCOKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPMLPLVRPEV	120		
QY	121	DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADRAACLLP	180		
DB	121	DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAAADRAACLLP	180		
QY	181	KLDELDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPAEFAEYSKLVTDLTK	240		
DB	181	KLDELDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPAEFAEYSKLVTDLTK	240		
QY	241	VHTECHGDLLECCADRADLAKYICENODSISSKLKECKEPLLEKSHCIAEVENDEMPA	300		
DB	241	VHTECHGDLLECCADRADLAKYICENODSISSKLKECKEPLLEKSHCIAEVENDEMPA	300		
QY	301	DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEVARRHPDYVSVLLRLAKTYETTLEKC	360		
DB	301	DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEVARRHPDYVSVLLRLAKTYETTLEKC	360		
QY	361	CAAADPHECYAKVDFEFPKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST	420		
DB	361	CAAADPHECYAKVDFEFPKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST	420		
QY	421	PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVNLQNLVLEHEKTPVSDRVTKCCTES	480		
DB	421	PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVNLQNLVLEHEKTPVSDRVTKCCTES	480		
QY	481	LVNRRPCFSALEVDVETVPKFEFNAETFTFHADICTLSEKRIKKQTALVELVKKPKAT	540		
DB	481	LVNRRPCFSALEVDVETVPKFEFNAETFTFHADICTLSEKRIKKQTALVELVKKPKAT	540		
QY	541	KEQLKAYMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL	585		
DB	541	KEQLKAYMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL	585		
RESULT 12					
ID	AAE12403				
XX	AAE12403 standard; Protein; 585 AA.				
AC	AAE12403;				
XX	18-DEC-2001 (first entry)				
DT	XX				
XX	Human albumin (HA).				
DE	XX				
XX	Human; albumin; HA; immune system disorder; transplant rejection;				
KW	blood related disorder; myocardial infarction; glomerulonephritis;				
KW	hyperproliferative disorder; childhood acute myeloid leukaemia;				
KW	renal cell carcinoma; cardiovascular disorder; vulvar; melanoma;				
KW	arrhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic;				
KW	neurological disease; Alzheimer's disease; endocrine disorder; measles;				
KW	pheochromocytoma; reproductive system disorder; neuroprotective; syphilis;				
KW	infectious disease; gastrointestinal disorder; wound healing; nystropia;				
KW	irritable bowel syndrome; HIV; human immunodeficiency virus infection;				
KW	cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant;				
KW	antiarthritic; antirheumatic; renal disorder; antimicrobial.				
OS	Homo sapiens.				
XX	Key				
FX	Domain				
FT	Location/Qualifiers				
FT	54..61				
FT	/label= Loop_I				
FT	76..89				
FT	/label= Loop_II				
FT	92..100				
FT	/label= Loop_III				
FT	170..176				
FT	/label= Loop_IV				
FT	247..252				
FT	/label= Loop_V				
FT	266..277				
FT	/label= Loop_VI				
FT	280..288				
FT	/label= Loop_VII				
FT	362..368				
FT	/label= Loop_VIII				
FT	439..447				
FT	/label= Loop_IX				
FT	461..475				
FT	/label= Loop_X				
FT	478..486				
FT	/label= Loop_XI				
FT	560..566				
FT	/label= Loop_XII				
XX	Sequence 585 AA;				

Domain 76..89 /label= Loop_II
Domain 92..100 /label= Loop_III
Domain 170..176 /label= Loop_IV
Domain 247..252 /label= Loop_V
Domain 266..277 /label= Loop_VI
Domain 280..288 /label= Loop_VII
Domain 362..368 /label= Loop_VIII
Domain 439..447 /label= Loop_IX
Domain 461..475 /label= Loop_X
Domain 478..486 /label= Loop_XI
Domain 560..566 /label= Loop_XII

WO200179480-A1.

25-OCT-2001.

12-APR-2001; 2001WO-US11991.

12-APR-2000; 2000US-229358P.

25-APR-2000; 2000US-199384P.

21-DEC-2000; 2000US-256931P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

WPI; 2001-616756/71.

N-PSDB; AAD20005.

Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human immunodeficiency virus) or infection.

Claim 1; Fig 9; 394pp; English.

The invention relates to human albumin (HA) fusion proteins and their corresponding nucleic acid sequences. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome), HIV (human immunodeficiency virus) infection and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is human albumin.

Query Match

Best Local Similarity 100.0%; Score 3103; DB 22; Length 585;

Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAHSEVAHRFDLGEENFKALVIAFAOYLOCCPEDHVKLVNEVTEFAKTCVADESAE 60
|||||

Db 1 DAHSEVAHRFDLGEENFKALVIAFAOYLOCCPEDHVKLVNEVTEFAKTCVADESAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQKQPERNECFLOHKDDNPNLRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQKQPERNECFLOHKDDNPNLRLVRPEV 120
Qy 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Qy 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWAVARLSQRPKAEFAEVSKLYTDLTK 240
Db 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWAVARLSQRPKAEFAEVSKLYTDLTK 240
Qy 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLEKCEKPLLEKSHGICIAEVENDMPA 300
Db 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLEKCEKPLLEKSHGICIAEVENDMPA 300
Qy 301 DLPSLAADFVESKQVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 360
Db 301 DLPSLAADFVESKQVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEKC 360
Qy 361 CAADPHECYAKVDFEKPVEEPQNLIKQNCLEFQELGEYKFQNALIVRYTKKVPQVST 420
Db 361 CAADPHECYAKVDFEKPVEEPQNLIKQNCLEFQELGEYKFQNALIVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCTES 480
Db 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCTES 480
Qy 481 LVNRRPCFSALEVDETYVPKEFAETFTPHADICTLSEKERQIKKQTALVELVKKHKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKEFAETFTPHADICTLSEKERQIKKQTALVELVKKHKPKAT 540
Qy 541 KEQLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585
Db 541 KEQLKAVMDDFAAFVEKCKCKADDDKTCFAEEGKKLVAAASQAALGL 585

RESULT 13

AAE08578

ID AAE08578 standard; Protein; 585 AA.

XX AC AAE08578;

XX DT 19-NOV-2001 (first entry)

XX DE Human serum albumin (HSA).

XX KW Human; albumin; cancer; cell proliferation; drug screening; biopsy.

XX OS Homo sapiens.

XX PN US6274305-B1.

XX PD 14-AUG-2001.

XX PF 19-DEC-1996; 96US-0769746.

XX PR 19-DEC-1996; 96US-0769746.

XX PA (TUFT) UNIV TUFTS.

XX PI Sonnenschein C, Soto AM;

XX DR WPI; 2001-540371/60.

XX DR N-PSDB; AAD11488.

PT Measuring human cell proliferation, useful in drug screening to
PT determine the potential for inhibiting cancer cell proliferation and
PT for evaluating biopsied tumors, comprises employing albumin-derived
PT peptide -
XX

PS Claim 1; Fig 1; 20pp; English.

XX The invention related to a method for testing cancer cells. The method is
 CC useful for measuring human cancer cell proliferation, particularly for
 CC determining the potential for inhibiting cancer cells proliferation using
 CC albumin-derived peptides. The invention is also useful for drug screening
 CC assays, as well as for evaluating biopsied tumours. The present sequence
 CC is human serum albumin (HSA) related to the invention.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 QY 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPFAEAEVSKLVTDLTG 240
 Db 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPFAEAEVSKLVTDLTG 240
 QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLK 360
 Db 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLK 360
 QY 361 CAADPHCEYAKVDFEFPKLVPEEPONLIKQNCLEFQELGKVFQNALVRYTKVPQVST 420
 Db 361 CAADPHCEYAKVDFEFPKLVPEEPONLIKQNCLEFQELGKVFQNALVRYTKVPQVST 420
 QY 421 PTLVEVSNLKGVSCKCKHPEAKRMPCAEDYLSVLNQLCVLHKTTPVSDRVTKCCYES 480
 Db 421 PTLVEVSNLKGVSCKCKHPEAKRMPCAEDYLSVLNQLCVLHKTTPVSDRVTKCCYES 480
 QY 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKRIQKQATLVELVHKPKAT 540
 Db 481 LVNRRPCFSALEVDYTPYKFEFNAETFTFHADICTLSEKRIQKQATLVELVHKPKAT 540
 QY 541 KEQLKAVMDDEFAAFVEKCKKADDETCFAEBGKLVAAASQAALGL 585
 Db 541 KEQLKAVMDDEFAAFVEKCKKADDETCFAEBGKLVAAASQAALGL 585

RESULT 14

ID ABG63321 standard; protein; 585 AA.

XX AC ABG63321;

XX DT 27-AUG-2002 (first entry)

XX DE Human serum albumin (HSA) protein.

XX Albumin fusion protein; therapeutic protein x; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytosolic; antifertility; antinflammatory; antitumor;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;

KW osteopathic; antiarthritic.

XX Homo sapiens.

PN WO200177137-A1.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-US11988.

XX PR 12-APR-2000; 2000US-229358P.

XX PR 25-APR-2000; 2000US-199384P.

XX PR 21-DEC-2000; 2000US-256931P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Haseltine WA;

XX DR WPI; 2002-010886/01.

XX DR N-PSDB; ABK93280.

XX PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -

XX PS Claim 1; Fig 15; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein x and human albumin (HA), also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein x. The albumin
 CC extends the shelf-life of protein x, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haematopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). The present sequence represents HSA
 CC (HA) protein.

XX SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 23; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1e-254;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db 1 DAHSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDDNPRLVLRPEV 120
 QY 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPFAEAEVSKLVTDLTG 240
 Db 181 KLDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRPFAEAEVSKLVTDLTG 240
 QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCERPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLK 360
 Db 301 DLPSLAADFVSKDCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLK 360
 QY 361 CAADPHCEYAKVDFEFPKLVPEEPONLIKQNCLEFQELGKVFQNALVRYTKVPQVST 420
 Db 361 CAADPHCEYAKVDFEFPKLVPEEPONLIKQNCLEFQELGKVFQNALVRYTKVPQVST 420

Db 361 CAAADPHCYAKVDFEKPVLVEEPQNLIKQNCLEFQOLGEYKFNQALLVRYTKVQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHETPVSDRYTKKCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHETPVSDRYTKKCTES 480
QY 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
Db 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585
Db 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585

RESULT 15
ABJ00986
ID ABJ00986 standard; Protein; 585 AA.
AC ABJ00986;
XX
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte stimulator protein binding peptide related protein.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Homo sapiens.
XX
PN WO200216411-A2.
XX
XX 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US25850.
XX
PR 18-AUG-2000; 2000US-226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide -
PT
XX
PS Disclosure; Page 379-382; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, infectious diseases, arteriosclerosis, inflammatory disorders,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a protein described
CC in the invention.
XX
SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 23; Length 585;

Best Local Similarity 100.0%; Pred. No. 1e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRFKDGLGENFKALVLIAPAOYLQOCPPEDHVKLVNEVTEFAKTCVADESA 60
Db 1 DAHSEVAHFRFKDGLGENFKALVLIAPAOYLQOCPPEDHVKLVNEVTEFAKTCVADESA 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNPNLRLVPEV 120
QY 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORPKAEFAEVSCLVTDLT 240
Db 181 KLDELDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORPKAEFAEVSCLVTDLT 240
QY 241 VHTCCCHGDLLECCADDDRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 300
Db 241 VHTCCCHGDLLECCADDDRADLAKYICENQDSISSKLECCCKPLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEK 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYSVVLLRLAKTYETTLEK 360
QY 361 CAAADPHCYAKVDFEKPVLVEEPQNLIKQNCLEFQOLGEYKFNQALLVRYTKVQVST 420
Db 361 CAAADPHCYAKVDFEKPVLVEEPQNLIKQNCLEFQOLGEYKFNQALLVRYTKVQVST 420
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHETPVSDRYTKKCTES 480
Db 421 PTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVNLQCLVLEHETPVSDRYTKKCTES 480
QY 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
Db 481 LVNRRPCFSALEVDYVVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585
Db 541 KEOLKAVMDDFAAFVEKCKKADDDKTCFAEEGKKLVAAASQAALGL 585

Search completed: April 24, 2003, 07:25:22
Job time : 81 secs